IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Application of	Group Art Unit: Unknown
Desnoyers, et al.	Examiner: Unknown
Serial No.: Filed herewith	
Filed: August 16, 2001	Express Mail No: EL 895 375 396 US Filed on August 16, 2001
For: *SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME*	

CERTIFICATE RE: SEQUENCE LISTING

RESPONSE UNDER 37 CFR § 1.821(f) and (g)

Box: Patent Application
Assistant Commissioner of Patents
Washington, D.C. 20231

Sir:

I hereby state that the Sequence Listing submitted herewith is submitted in paper copy and a computer-readable diskette, and that the information recorded in computer readable form is identical to the written sequence listing. I further state that this submission includes no new matter.

Respectfully submitted,

GENENTECH, INC.

Date: August 16, 2001

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09157

PATENT TRADEMARK OFFICE

Revised (10/18/95)

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     Zhang,Zemin

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                20                  25                  30

Gln Thr Gly Gly Leu Pro Pro Asp Cys Ser Lys Cys Cys His Gly
                35                  40                  45

Asp Tyr Ser Phe Arg Gly Tyr Gln Gly Pro Pro Gly Pro Pro Gly
                50                  55                  60

Pro Pro Gly Ile Pro Gly Asn His Gly Asn Asn Gly Asn Asn Gly
                65                  70                  75

Ala Thr Gly His Glu Gly Ala Lys Gly Glu Lys Gly Asp Lys Gly
                80                  85                  90

Asp Leu Gly Pro Arg Gly Glu Arg Gly Gln His Gly Pro Lys Gly
                95                  100                 105

Glu Lys Gly Tyr Pro Gly Ile Pro Pro Glu Leu Gln Ile Ala Phe
                110                 115                 120

Met Ala Ser Leu Ala Thr His Phe Ser Asn Gln Asn Ser Gly Ile
                125                 130                 135

Ile Phe Ser Ser Val Glu Thr Asn Ile Gly Asn Phe Phe Asp Val
                140                 145                 150
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5

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Met Thr Gly Arg Phe Gly Ala Pro Val Ser Gly Val Tyr Phe Phe
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Thr Phe Ser Met Met Lys His Glu Asp Val Glu Glu Val Tyr Val
                170                 175                 180

Tyr Leu Met His Asn Gly Asn Thr Val Phe Ser Met Tyr Ser Tyr
                185                 190                 195

Glu Met Lys Gly Lys Ser Asp Thr Ser Ser Asn His Ala Val Leu
                200                 205                 210

Lys Leu Ala Lys Gly Asp Glu Val Trp Leu Arg Met Gly Asn Gly
                215                 220                 225

Ala Leu His Gly Asp His Gln Arg Phe Ser Thr Phe Ala Gly Phe
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Leu Leu Phe Glu Thr Lys
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Leu Asp Gly Phe Arg Ser Asp Tyr Ile Ser Asp Glu Ala Leu Glu
                 35                  40                  45

Ser Leu Pro Gly Phe Lys Glu Ile Val Ser Arg Gly Val Lys Val
                 50                  55                  60

Asp Tyr Leu Thr Pro Asp Phe Pro Ser Leu Ser Tyr Pro Asn Tyr
                 65                  70                  75

Tyr Thr Leu Met Thr Gly Arg His Cys Glu Val His Gln Met Ile
                 80                  85                  90

Gly Asn Tyr Met Trp Asp Pro Thr Thr Asn Lys Ser Phe Asp Ile
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Gly Val Asn Lys Asp Ser Leu Met Pro Leu Trp Trp Asn Gly Ser
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8

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Pro Thr Tyr Cys Leu Glu Tyr Lys Asn Val Pro Thr Asp Ile Asn
                    155   160   165

Phe Ala Asn Ala Val Ser Asp Ala Leu Asp Ser Phe Lys Ser Gly
                    170   175   180

Arg Ala Asp Leu Ala Ala Ile Tyr His Glu Arg Ile Asp Val Glu
                    185   190   195

Gly His His Tyr Gly Pro Ala Ser Pro Gln Arg Lys Asp Ala Leu
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Lys Ala Val Asp Thr Val Leu Lys Tyr Met Thr Lys Trp Ile Gln
                    215   220   225

Glu Arg Gly Leu Gln Asp Arg Leu Asn Val Ile Ile Phe Ser Asp
                    230   235   240

His Gly Met Thr Asp Ile Phe Trp Met Asp Lys Val Ile Glu Leu
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Asn Lys Tyr Ile Ser Leu Asn Asp Leu Gln Gln Val Lys Asp Arg
                    260   265   270

Gly Pro Val Val Ser Leu Trp Pro Ala Pro Gly Lys His Ser Glu
                    275   280   285

Ile Tyr Asn Lys Leu Ser Thr Val Glu His Met Thr Val Tyr Glu
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Lys Glu Ala Ile Pro Ser Arg Phe Tyr Tyr Lys Lys Gly Lys Phe
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Val Ser Pro Leu Thr Leu Val Ala Asp Glu Gly Trp Phe Ile Thr
                    320   325   330

Glu Asn Arg Glu Met Leu Pro Phe Trp Met Asn Ser Thr Gly Arg
                    335   340   345

Arg Glu Gly Trp Gln Arg Gly Trp His Gly Tyr Asp Asn Glu Leu
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Met Asp Met Arg Gly Ile Phe Leu Ala Phe Gly Pro Asp Phe Lys
                    365   370   375

Ser Asn Phe Arg Ala Ala Pro Ile Arg Ser Val Asp Val Tyr Asn
                    380   385   390

Val Met Cys Asn Val Val Gly Ile Thr Pro Leu Pro Asn Asn Gly
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His Gly Thr Pro His Cys Tyr Ser Ala Glu Glu Leu Pro Leu Gly
                35                  40                  45

Gln Ala Pro Pro His Leu Leu Ala Arg Gly Ala Lys Trp Gly Gln
                50                  55                  60

Ala Leu Pro Val Ala Leu Val Ser Ser Leu Glu Ala Ala Ser His
                65                  70                  75

Arg Gly Arg His Glu Arg Pro Ser Ala Thr Thr Gln Cys Pro Val
                80                  85                  90

Leu Arg Pro Glu Glu Val Leu Glu Ala Asp Thr His Gln Arg Ser
                95                  100                 105

Ile Ser Pro Trp Arg Tyr Arg Val Asp Thr Asp Glu Asp Arg Tyr
                110                 115                 120

Pro Gln Lys Leu Ala Phe Ala Glu Cys Leu Cys Arg Gly Cys Ile
                125                 130                 135

Asp Ala Arg Thr Gly Arg Glu Thr Ala Ala Leu Asn Ser Val Arg
                140                 145                 150

Leu Leu Gln Ser Leu Leu Val Leu Arg Arg Arg Pro Cys Ser Arg
                155                 160                 165

Asp Gly Ser Gly Leu Pro Thr Pro Gly Ala Phe Ala Phe His Thr
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Glu Phe Ile His Val Pro Val Gly Cys Thr Cys Val Leu Pro Arg
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Ser Val
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<213> Homo Sapien

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Phe Gly Gly Cys Ser His Gly Ser Arg Cys Leu Arg Asp Ser Thr
                35   40   45

His Cys Val Thr Thr Ala Thr Arg Val Leu Ser Asn Thr Glu Asp
                50   55   60

Leu Pro Leu Val Thr Lys Met Cys His Ile Gly Cys Pro Asp Ile
                65   70   75

Pro Ser Leu Gly Leu Gly Pro Tyr Val Ser Ile Ala Cys Cys Gln
                80   85   90

Thr Ser Leu Cys Asn His Asp
                95

<210> 17
<211> 2570
<212> DNA
<213> Homo Sapien

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attcagagtc gcgggctgcg ccctgggcag aggccgccct cgctccacgc 350

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13

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actgtggatt tcaaagagta ccagaaaaga aagtggcatg gaagtataat 1200

aactcattga cttggttcca gaattttgta attctggatc tgtataagga 1250

atggcatcag aacaatagct tggaatggct tgaaatcaca aaggatctgc 1300

aagatgaact gtaagctccc ccttgaggca aatattaaag taatttttat 1350

atgtctatta tttcatttaa agaatatgct gtgctaataa tggagtgaga 1400

catgcttatt ttgctaaagg atgcacccaa acttcaaact tcaagcaaat 1450

gaaatggaca atgcagataa agttgttatc aacacgtcgg gagtatgtgt 1500

gttagaagca attccttta tttctttcac ctttcataag ttgttatcta 1550

gtcaatgtaa tgtatattgt attgaaattt acagtgtgca aaagtatttt 1600

acctttgcat aagtgtttga taaaaatgaa ctgttctaat atttattttt 1650

atggcatctc atttttcaat acatgctctt ttgattaaag aaacttatta 1700

ctgttgtcaa ctgaattcac acacacacaa atatagtacc atagaaaaag 1750

tttgtttttct cgaaataatt catctttcag cttctctgct tttggtcaat 1800

gtctaggaaa tctcttcaga aataagaagc tatttcatta agtgtgatat 1850

aaacctcctc aaacatttta cttagaggca aggattgtct aatttcaatt 1900

gtgcaagaca tgtgccttat aattattttt agcttaaaat taaacagatt 1950

ttgtaataat gtaactttgt taataggtgc ataaacacta atgcagtcaa 2000

tttgaacaaa agaagtgaca tacacaatat aaatcatatg tcttcacacg 2050

ttgcctatat aatgagaagc agctctctga gggttctgaa atcaatgtgg 2100

tccctctctt gcccactaaa caaagatggt tgttcggggt ttgggattga 2150
```

14

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cactggaggc agatagttgc aaagttagtc taaggtttcc ctagctgtat 2200

ttagcctctg actatattag tatacaaaga ggtcatgtgg ttgagaccag 2250

gtgaatagtc actatcagtg tggagacaag cacagcacac agacatttta 2300

ggaaggaaag gaactacgaa atcgtgtgaa aatgggttgg aacccatcag 2350

tgatcgcata ttcattgatg agggtttgct tgagatagaa aatggtggct 2400

cctttctgtc ttatctccta gtttcttcaa tgcttacgcc ttgttcttct 2450

caagagaaag ttgtaactct ctggtcttca tatgtccctg tgctcctttt 2500

aaccaaataa agagttcttg tttctggggg aaaaaaaaaa aaaaaaaaaa 2550

aaaaaaaaaa aaaaaaaaaa 2570
```

<210> 18
<211> 273
<212> PRT
<213> Homo Sapien

<400> 18

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Met Ser Arg Val Val Ser Leu Leu Leu Gly Ala Ala Leu Leu Cys
 1               5                  10                      15

Gly His Gly Ala Phe Cys Arg Arg Val Val Ser Gly Gln Lys Val
                20                  25                      30

Cys Phe Ala Asp Phe Lys His Pro Cys Tyr Lys Met Ala Tyr Phe
                35                  40                      45

His Glu Leu Ser Ser Arg Val Ser Phe Gln Glu Ala Arg Leu Ala
                50                  55                      60

Cys Glu Ser Glu Gly Gly Val Leu Leu Ser Leu Glu Asn Glu Ala
                65                  70                      75

Glu Gln Lys Leu Ile Glu Ser Met Leu Gln Asn Leu Thr Lys Pro
                80                  85                      90

Gly Thr Gly Ile Ser Asp Gly Asp Phe Trp Ile Gly Leu Trp Arg
                95                  100                     105

Asn Gly Asp Gly Gln Thr Ser Gly Ala Cys Pro Asp Leu Tyr Gln
                110                 115                     120

Trp Ser Asp Gly Ser Asn Ser Gln Tyr Arg Asn Trp Tyr Thr Asp
                125                 130                     135

Glu Pro Ser Cys Gly Ser Glu Lys Cys Val Val Met Tyr His Gln
                140                 145                     150

Pro Thr Ala Asn Pro Gly Leu Gly Gly Pro Tyr Leu Tyr Gln Trp
                155                 160                     165

Asn Asp Asp Arg Cys Asn Met Lys His Asn Tyr Ile Cys Lys Tyr
```

15
```

```
                     170                    175                    180
    Glu Pro Glu Ile Asn Pro Thr Ala Pro Val Glu Lys Pro Tyr Leu
                     185                    190                    195

    Thr Asn Gln Pro Gly Asp Thr His Gln Asn Val Val Val Thr Glu
                     200                    205                    210

    Ala Gly Ile Ile Pro Asn Leu Ile Tyr Val Val Ile Pro Thr Ile
                     215                    220                    225

    Pro Leu Leu Leu Leu Ile Leu Val Ala Phe Gly Thr Cys Cys Phe
                     230                    235                    240

    Gln Met Leu His Lys Ser Lys Gly Arg Thr Lys Thr Ser Pro Asn
                     245                    250                    255

    Gln Ser Thr Leu Trp Ile Ser Lys Ser Thr Arg Lys Glu Ser Gly
                     260                    265                    270

    Met Glu Val


<210> 19
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 19
 caccaaccaa ctgccaatcc tggc 24

<210> 20
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 20
 accacattct gatgggtgtc tcctgg 26

<210> 21
<211> 49
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 21
 gggtccctac ctttaccagt ggaatgatga caggtgtaac atgaagcac 49

<210> 22
<211> 3824
```

<212> DNA
<213> Homo Sapien

<400> 22
ggagaatgga gagagcagtg agagtggagt ccgggtcct ggtcggggtg 50

gtctgtctgc tcctggcatg ccctgccaca gccactgggc ccgaagttgc 100

tcagcctgaa gtagacacca ccctgggtcg tgtgcgaggc cggcaggtgg 150

gcgtgaaggg cacagaccgc cttgtgaatg tctttctggg cattccattt 200

gcccagccgc cactgggccc tgaccggttc tcagccccac acccagcaca 250

gccctgggag ggtgtgcggg atgccagcac tgcgccccca atgtgcctac 300

aagacgtgga gagcatgaac agcagcagat ttgtcctcaa cggaaaacag 350

cagatcttct ccgtttcaga ggactgcctg gtcctcaacg tctatagccc 400

agctgaggtc cccgcagggt ccggtaggcc ggtcatggta tgggtccatg 450

gaggcgctct gataactggc gctgccacct cctacgatgg atcagctctg 500

gctgcctatg gggatgtggt cgtggttaca gtccagtacc gccttggggt 550

ccttggcttc ttcagcactg gagatgagca tgcacctggc aaccagggct 600

tcctagatgt ggtagctgct ttgcgctggg tgcaagaaaa catcgccccc 650

ttcggggtg acctcaactg tgtcactgtc tttggtggat ctgccggtgg 700

gagcatcatc tctggcctgg tcctgtcccc agtggctgca gggctgttcc 750

acagagccat cacacagagt ggggtcatca ccaccccagg gatcatcgac 800

tctcaccctt ggccctagc tcagaaaatc gcaaacacct ggcctgcag 850

ctccagctcc ccggctgaga tggtgcagtg ccttcagcag aaagaaggag 900

aagagctggt ccttagcaag aagctgaaaa atactatcta tcctctcacc 950

gttgatggca ctgtcttccc caaaagcccc aaggaactcc tgaaggagaa 1000

gcccttccac tctgtgccct tcctcatggg tgtcaacaac catgagttca 1050

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agccgggagg acatgctggc catctcaaca cccgtcttga ccagtctgga 1150

tgtgccccct gagatgatgc ccaccgtcat agatgaatac ctaggaagca 1200

actcggacgc acaagccaaa tgccaggcgt tccaggaatt catgggtgac 1250

gtattcatca atgttcccac cgtcagtttt tcaagatacc ttcgagattc 1300

tggaagccct gtcttttct atgagttcca gcatcgaccc agttcttttg 1350

17

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cgaagatcaa acctgcctgg gtgaaggctg atcatggggc cgagggtgct 1400

tttgtgttcg gaggtccctt cctcatggac gagagctccc gcctggcctt 1450

tccagaggcc acagaggagg agaagcagct aagcctcacc atgatggccc 1500

agtggaccca ctttgcccgg acaggggacc ccaatagcaa ggctctgcct 1550

ccttggcccc aattcaacca ggcggaacaa tatctggaga tcaacccagt 1600

gccacgggcc ggacagaagt tcagggaggc ctggatgcag ttctggtcag 1650

agacgctccc cagcaagata caacagtggc accagaagca gaagaacagg 1700

aaggcccagg aggacctctg aggccaggcc tgaaccttct tggctggggc 1750

aaaccactct tcaagtggtg gcagagtccc agcacggcag cccgcctctc 1800

cccctgctga gactttaatc tccaccagcc cttaaagtgt cggccgctct 1850

gtgactggag ttatgctctt ttgaaatgtc acaaggccgc ctcccacctc 1900

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gtgagtgagt gaaacacaga atatgggaat ggcagctgct gaacttgaac 2250

ccagagcctt caggtgccaa agccatactc aggcccccac cgacattgtc 2300

caccctggcc agaagggtgc atgccaatgg cagagacctg ggatgggaga 2350

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aggccagggg agggcatctg gaccagggca tccgtcgggc tattgtcaca 2700

gagaaaagaa gagacccacc cactcgggct gcaaaaggtg aaaagcacca 2750

agaggttttc agatggaagt gagaggtgac agtgtgctgg cagccctcac 2800
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18

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agccctcgct tgctctccct gccgcctctg cctgggctcc cactttggca 2850

gcacttgagg agcccttcaa cccgccgctg cactgtagga gcccctttct 2900

gggctggcca aggccggagc cagctccctc agcttgcggg gaggtgcgga 2950

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agtgagttcc gggtgggcgt gggctcggcg gggccccact cagagcagct 3050

ggccggcccc aggcagtgag ggccttagca cctgggccag cagctgctgt 3100

gctcgatttc tcgctgggcc ttagctgcct ccccgcgggg cagggctcgg 3150

gacctgcagc cctccatgcc tgaccctccc cccacccccc gtgggctcct 3200

gtgcggccgg agcctcccca aggagcgccg ccccctgctc cacagcgccc 3250

agtcccatcg accacccaag ggctgaggag tgcgggtgca cagcgcggga 3300

ctggcaggca gctccacctg ctgccccagt gctggatcca ctgggtgaag 3350

ccagctgggc tcctgagtct ggtggggact tggagaacct ttatgtctag 3400

ctaagggatt gtaaatacac cgatgggcac tctgtatcta gctcaaggtt 3450

tgtaaacaca ccaatcagca ccctgtgtct agctcagtgt ttgtgaatgc 3500

accaatccac actctgtatc tggctactct ggtggggact tggagaacct 3550

ttgtgtccac actctgtatc tagctaatct agtggggatg tggagaacct 3600

ttgtgtctag ctcagggatc gtaaacgcac caatcagcac cctgtcaaaa 3650

cagaccactt gactctctgt aaaatggacc aatcagcagg atgtgggtgg 3700

ggcgagacaa gagaataaaa gcaggctgcc tgagccagca gtgacaaccc 3750

ccctcgggtc ccctcccacg ccgtggaagc tttgttcttt cgctctttgc 3800

aataaatctt gctactgccc aaaa 3824
```

<210> 23
<211> 571
<212> PRT
<213> Homo Sapien

<400> 23

```
Met Glu Arg Ala Val Arg Val Glu Ser Gly Val Leu Val Gly Val
 1               5                   10                  15

Val Cys Leu Leu Leu Ala Cys Pro Ala Thr Ala Thr Gly Pro Glu
                20                  25                  30

Val Ala Gln Pro Glu Val Asp Thr Thr Leu Gly Arg Val Arg Gly
                35                  40                  45

Arg Gln Val Gly Val Lys Gly Thr Asp Arg Leu Val Asn Val Phe
```

19

Leu Gly Ile Pro Phe Ala Gln Pro Pro Leu Gly Pro Asp Arg Phe
   65   70   75

Ser Ala Pro His Pro Ala Gln Pro Trp Glu Gly Val Arg Asp Ala
   80   85   90

Ser Thr Ala Pro Pro Met Cys Leu Gln Asp Val Glu Ser Met Asn
   95   100   105

Ser Ser Arg Phe Val Leu Asn Gly Lys Gln Gln Ile Phe Ser Val
   110   115   120

Ser Glu Asp Cys Leu Val Leu Asn Val Tyr Ser Pro Ala Glu Val
   125   130   135

Pro Ala Gly Ser Gly Arg Pro Val Met Val Trp Val His Gly Gly
   140   145   150

Ala Leu Ile Thr Gly Ala Ala Thr Ser Tyr Asp Gly Ser Ala Leu
   155   160   165

Ala Ala Tyr Gly Asp Val Val Val Val Thr Val Gln Tyr Arg Leu
   170   175   180

Gly Val Leu Gly Phe Phe Ser Thr Gly Asp Glu His Ala Pro Gly
   185   190   195

Asn Gln Gly Phe Leu Asp Val Val Ala Ala Leu Arg Trp Val Gln
   200   205   210

Glu Asn Ile Ala Pro Phe Gly Gly Asp Leu Asn Cys Val Thr Val
   215   220   225

Phe Gly Gly Ser Ala Gly Gly Ser Ile Ile Ser Gly Leu Val Leu
   230   235   240

Ser Pro Val Ala Ala Gly Leu Phe His Arg Ala Ile Thr Gln Ser
   245   250   255

Gly Val Ile Thr Thr Pro Gly Ile Ile Asp Ser His Pro Trp Pro
   260   265   270

Leu Ala Gln Lys Ile Ala Asn Thr Leu Ala Cys Ser Ser Ser Ser
   275   280   285

Pro Ala Glu Met Val Gln Cys Leu Gln Gln Lys Glu Gly Glu Glu
   290   295   300

Leu Val Leu Ser Lys Lys Leu Lys Asn Thr Ile Tyr Pro Leu Thr
   305   310   315

Val Asp Gly Thr Val Phe Pro Lys Ser Pro Lys Glu Leu Leu Lys
   320   325   330

Glu Lys Pro Phe His Ser Val Pro Phe Leu Met Gly Val Asn Asn
   335   340   345

```
His Glu Phe Ser Trp Leu Ile Pro Arg Gly Trp Gly Leu Leu Asp
            350                 355                 360

Thr Met Glu Gln Met Ser Arg Glu Asp Met Leu Ala Ile Ser Thr
            365                 370                 375

Pro Val Leu Thr Ser Leu Asp Val Pro Pro Glu Met Met Pro Thr
            380                 385                 390

Val Ile Asp Glu Tyr Leu Gly Ser Asn Ser Asp Ala Gln Ala Lys
            395                 400                 405

Cys Gln Ala Phe Gln Glu Phe Met Gly Asp Val Phe Ile Asn Val
            410                 415                 420

Pro Thr Val Ser Phe Ser Arg Tyr Leu Arg Asp Ser Gly Ser Pro
            425                 430                 435

Val Phe Phe Tyr Glu Phe Gln His Arg Pro Ser Ser Phe Ala Lys
            440                 445                 450

Ile Lys Pro Ala Trp Val Lys Ala Asp His Gly Ala Glu Gly Ala
            455                 460                 465

Phe Val Phe Gly Gly Pro Phe Leu Met Asp Glu Ser Ser Arg Leu
            470                 475                 480

Ala Phe Pro Glu Ala Thr Glu Glu Glu Lys Gln Leu Ser Leu Thr
            485                 490                 495

Met Met Ala Gln Trp Thr His Phe Ala Arg Thr Gly Asp Pro Asn
            500                 505                 510

Ser Lys Ala Leu Pro Pro Trp Pro Gln Phe Asn Gln Ala Glu Gln
            515                 520                 525

Tyr Leu Glu Ile Asn Pro Val Pro Arg Ala Gly Gln Lys Phe Arg
            530                 535                 540

Glu Ala Trp Met Gln Phe Trp Ser Glu Thr Leu Pro Ser Lys Ile
            545                 550                 555

Gln Gln Trp His Gln Lys Gln Lys Asn Arg Lys Ala Gln Glu Asp
            560                 565                 570

Leu


<210> 24
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 24
 gcaaagctct gcctccttgg cc 22
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21

```
<210> 25
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 25
 gggtggactg tgctctaatg gacgc 25

<210> 26
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 26
 cgtggcactg ggttgatc 18

<210> 27
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 27
 gatgcagttc tggtcagaga cgctccccag caagatacaa cagtg 45

<210> 28
<211> 1342
<212> DNA
<213> Homo Sapien

<400> 28
 catggagcct cttgcagctt acccgctaaa atgttccggg cccagagcaa 50

 aggtatttgc agttttgctg tctatagttc tatgcacagt aacgctattt 100

 cttctacaac taaaattcct caaacctaaa atcaacagct tttatgcctt 150

 tgaagtgaag gatgcaaaag gaagaactgt ttctctggaa aagtataaag 200

 gcaaagtttc actagttgta aacgtggcca gtgactgcca actcacagac 250

 agaaattact tagggctgaa ggaactgcac aaagagtttg gaccatccca 300

 cttcagcgtg ttggcttttc cctgcaatca gtttggagaa tcggagcccc 350

 gcccaagcaa ggaagtagaa tcttttgcaa gaaaaaacta cggagtaact 400

 ttccccatct tccacaagat taagattcta ggatctgaag gagaacctgc 450

 atttagattt cttgttgatt cttcaaagaa ggaaccaagg tggaattttt 500
```

22

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ggaagtatct tgtcaaccct gagggtcaag ttgtgaagtt ctggaggcca 550

gaggagccca ttgaagtcat caggcctgac atagcagctc tggttagaca 600

agtgatcata aaaaagaaag aggatctatg agaatgccat tgcgtttcta 650

atagaacaga gaaatgtctc catgagggtt tggtctcatt ttaaacattt 700

tttttttgga gacagtgtct cactctgtca cccaggctgg agtgcagtag 750

tgcgttctca gctcattgca acctctgcct ttttaaacat gctattaaat 800

gtggcaatga aggatttttt tttaatgtta tcttgctatt aagtggtaat 850

gaatgttccc aggatgagga tgttacccaa agcaaaaatc aagagtagcc 900

aaagaatcaa catgaaatat attaactact tcctctgacc atactaaaga 950

attcagaata cacagtgacc aatgtgcctc aatatcttat tgttcaactt 1000

gacattttct aggactgtac ttgatgaaaa tgccaacaca ctagaccact 1050

ctttggattc aagagcactg tgtatgactg aaatttctgg ataactgta 1100

aatggttatg ttaatggaat aaaacacaaa tgttgaaaaa tgtaaaatat 1150

atatacatag attcaaatcc ttatatatgt atgcttgttt tgtgtacagg 1200

attttgtttt ttctttttaa gtacaggttc ctagtgtttt actataactg 1250

tcactatgta tgtaactgac atatataaat agtcatttat aaatgaccgt 1300

attataacat ttgaaaaagt cttcatcaaa aaaaaaaaa aa 1342

<210> 29
<211> 209
<212> PRT
<213> Homo Sapien

<400> 29
Met Glu Pro Leu Ala Ala Tyr Pro Leu Lys Cys Ser Gly Pro Arg
 1               5                  10                  15

Ala Lys Val Phe Ala Val Leu Leu Ser Ile Val Leu Cys Thr Val
                20                  25                  30

Thr Leu Phe Leu Leu Gln Leu Lys Phe Leu Lys Pro Lys Ile Asn
                35                  40                  45

Ser Phe Tyr Ala Phe Glu Val Lys Asp Ala Lys Gly Arg Thr Val
                50                  55                  60

Ser Leu Glu Lys Tyr Lys Gly Lys Val Ser Leu Val Val Asn Val
                65                  70                  75

Ala Ser Asp Cys Gln Leu Thr Asp Arg Asn Tyr Leu Gly Leu Lys
                80                  85                  90
```

23

```
Glu Leu His Lys Glu Phe Gly Pro Ser His Phe Ser Val Leu Ala
                95                  100                 105

Phe Pro Cys Asn Gln Phe Gly Glu Ser Glu Pro Arg Pro Ser Lys
                110                 115                 120

Glu Val Glu Ser Phe Ala Arg Lys Asn Tyr Gly Val Thr Phe Pro
                125                 130                 135

Ile Phe His Lys Ile Lys Ile Leu Gly Ser Glu Gly Glu Pro Ala
                140                 145                 150

Phe Arg Phe Leu Val Asp Ser Ser Lys Lys Glu Pro Arg Trp Asn
                155                 160                 165

Phe Trp Lys Tyr Leu Val Asn Pro Glu Gly Gln Val Val Lys Phe
                170                 175                 180

Trp Arg Pro Glu Glu Pro Ile Glu Val Ile Arg Pro Asp Ile Ala
                185                 190                 195

Ala Leu Val Arg Gln Val Ile Ile Lys Lys Lys Glu Asp Leu
                200                 205
```

<210> 30
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 30
 atcctccaac atggagcctc ttgc 24

<210> 31
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 31
 gtatcttgtc aaccctgagg 20

<210> 32
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 32
 taaccagagc tgctatgtca ggcc 24

<210> 33

24

<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 33
aggcaaagtt tcactagttg taaacgtggc cagtgactgc caactcacag 50

<210> 34
<211> 3721
<212> DNA
<213> Homo Sapien

<400> 34
tgtcgcctgg ccctcgccat gcagaccccg cgagcgtccc ctccccgccc 50

ggccctcctg cttctgctgc tgctactggg gggcgcccac ggcctctttc 100

ctgaggagcc gccgccgctt agcgtggccc ccagggacta cctgaaccac 150

tatcccgtgt ttgtgggcag cgggcccgga cgcctgaccc ccgcagaagg 200

tgctgacgac ctcaacatcc agcgagtcct gcgggtcaac aggacgctgt 250

tcattgggga cagggacaac ctctaccgcg tagagctgga gccccccacg 300

tccacggagc tgcggtacca gaggaagctg acctggagat ctaaccccag 350

cgacataaac gtgtgtcgga tgaagggcaa acaggagggc gagtgtcgaa 400

acttcgtaaa ggtgctgctc cttcgggacg agtccacgct ctttgtgtgc 450

ggttccaacg ccttcaaccc ggtgtgcgcc aactacagca tagacaccct 500

gcagcccgtc ggagacaaca tcagcggtat ggcccgctgc ccgtacgacc 550

ccaagcacgc caatgttgcc ctcttctctg acgggatgct cttcacagct 600

actgttaccg acttcctagc cattgatgct gtcatctacc gcagcctcgg 650

ggacaggccc accctgcgca ccgtgaaaca tgactccaag tggttcaaag 700

agccttactt tgtccatgcg gtggagtggg gcagccatgt ctacttcttc 750

ttccgggaga ttgcgatgga gtttaactac ctggagaagg tggtggtgtc 800

ccgcgtggcc cgagtgtgca gaacgacgt gggaggctcc ccccgcgtgc 850

tggagaagca gtggacgtcc ttcctgaagg cgcggctcaa ctgctctgta 900

cccggagact cccatttcta cttcaacgtg ctgcaggctg tcacgggcgt 950

ggtcagcctc ggggggccggc ccgtggtcct ggccgttttt tccacgccca 1000

gcaacagcat ccctggctcg gctgtctgcg cctttgacct gacacaggtg 1050

25

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gcagctgtgt ttgaaggccg cttccgagag cagaagtccc ccgagtccat 1100

ctggacgccg gtgccggagg atcaggtgcc tcgaccccgg cccgggtgct 1150

gcgcagcccc cgggatgcag tacaatgcct ccagcgcctt gccggatgac 1200

atcctcaact ttgtcaagac ccaccctctg atggacgagg cggtgccctc 1250

gctgggccat gcgccctgga tcctgcggac cctgatgagg caccagctga 1300

ctcgagtggc tgtggacgtg ggagccggcc cctggggcaa ccagaccgtt 1350

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caatgccagc acctcaggga cgtctgggct cagtgtcttc ctggaggagt 1450

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ggctgccttc ccccgctgcg tggtccgagt gcctgtggct cgctgccagc 1600

agtactcggg gtgtatgaag aactgtatcg gcagtcagga cccctactgc 1650

gggtgggccc ccgacggctc ctgcatcttc ctcagcccgg gcaccagagc 1700

cgcctttgag caggacgtgt ccggggccag cacctcaggc ttaggggact 1750

gcacaggact cctgcgggcc agcctctccg aggaccgcgc ggggctggtg 1800

tcggtgaacc tgctggtaac gtcgtcggtg gcggccttcg tggtgggagc 1850

cgtggtgtcc ggcttcagcg tgggctggtt cgtgggcctc cgtgagcggc 1900

gggagctggc ccggcgcaag gacaaggagg ccatcctggc gcacggggcg 1950

ggcgaggcgg tgctgagcgt cagccgcctg ggcgagcgca gggcgcaggg 2000

tcccgggggc cggggcggag gcggtggcgg tggcgccggg gttcccccgg 2050

aggccctgct ggcgcccctg atgcagaacg ctgggccaa ggccacgctg 2100

ctgcagggcg ggccccacga cctggactcg gggctgctgc ccacgcccga 2150

gcagacgccg ctgccgcaga agcgcctgcc cactccgcac ccgcaccccc 2200

acgccctggg cccccgcgcc tgggaccacg gccacccccct gctcccggcc 2250

tccgcttcat cctccctcct gctgctggcg cccgccgggg ccccgagca 2300

gccccccgcg cctggggagc cgacccccga cggccgcctc tatgctgccc 2350

ggcccggccg cgcctcccac ggcgacttcc cgctcacccc ccacgccagc 2400

ccggaccgcc ggcgggtggt gtccgcgccc acgggcccct ggacccagc 2450

ctcagccgcc gatggcctcc cgcggccctg gagcccgccc ccgacgggca 2500
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26

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gcctgaggag gccactgggc ccccacgccc ctccggccgc caccctgcgc 2550

cgcacccaca cgttcaacag cggcgaggcc cggcctgggg accgccaccg 2600

cggctgccac gcccggccgg gcacagactt ggcccacctc ctcccctatg 2650

ggggggcgga caggactgcg ccccccgtgc cctaggccgg gggcccccccg 2700

atgccttggc agtgccagcc acgggaacca ggagcgagag acggtgccag 2750

aacgccgggg cccgggggcaa ctccgagtgg gtgctcaagt ccccccccgcg 2800

acccacccgc ggagtggggg gccccctccg ccacaaggaa gcacaaccag 2850

ctcgccctcc ccctacccgg ggccgcagga cgctgagacg gtttgggggt 2900

gggtgggcgg gaggactttg ctatggattt gaggttgacc ttatgcgcgt 2950

aggttttggt ttttttttgc agttttggtt tcttttgcgg ttttctaacc 3000

aattgcacaa ctccgttctc ggggtggcgg caggcagggg aggcttggac 3050

gccggtgggg aatggggggc cacagctgca gacctaagcc ctcccccacc 3100

cctggaaagg tccctccccca acccaggccc ctggcgtgtg tgggtgtgcg 3150

tgcgtgtgcg tgccgtgttc gtgtgcaagg ggccggggag gtgggcgtgt 3200

gtgtgcgtgc cagcgaaggc tgctgtgggc gtgtgtgtca agtgggccac 3250

gcgtgcaggg tgtgtgtcca cgagcgacga tcgtggtggc cccagcggcc 3300

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ccatgcatgc cacgtggctg gctgggtcct ctgccctctt tggagtttgc 3650

ctcccccagc cccctcccca tcaataaaac tctgtttaca accaaaaaaa 3700

aaaaaaaaaa aaaaaaaaaa a 3721
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<210> 35
<211> 888
<212> PRT
<213> Homo Sapien

<400> 35
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 Met Gln Thr Pro Arg Ala Ser Pro Pro Pro Ala Leu Leu Leu
  1               5                  10                  15
```

27

Leu Leu Leu Leu Leu Gly Gly Ala His Gly Leu Phe Pro Glu Glu
                20   25   30

Pro Pro Pro Leu Ser Val Ala Pro Arg Asp Tyr Leu Asn His Tyr
                35   40   45

Pro Val Phe Val Gly Ser Gly Pro Gly Arg Leu Thr Pro Ala Glu
                50   55   60

Gly Ala Asp Asp Leu Asn Ile Gln Arg Val Leu Arg Val Asn Arg
                65   70   75

Thr Leu Phe Ile Gly Asp Arg Asp Asn Leu Tyr Arg Val Glu Leu
                80   85   90

Glu Pro Pro Thr Ser Thr Glu Leu Arg Tyr Gln Arg Lys Leu Thr
                95   100   105

Trp Arg Ser Asn Pro Ser Asp Ile Asn Val Cys Arg Met Lys Gly
                110   115   120

Lys Gln Glu Gly Glu Cys Arg Asn Phe Val Lys Val Leu Leu Leu
                125   130   135

Arg Asp Glu Ser Thr Leu Phe Val Cys Gly Ser Asn Ala Phe Asn
                140   145   150

Pro Val Cys Ala Asn Tyr Ser Ile Asp Thr Leu Gln Pro Val Gly
                155   160   165

Asp Asn Ile Ser Gly Met Ala Arg Cys Pro Tyr Asp Pro Lys His
                170   175   180

Ala Asn Val Ala Leu Phe Ser Asp Gly Met Leu Phe Thr Ala Thr
                185   190   195

Val Thr Asp Phe Leu Ala Ile Asp Ala Val Ile Tyr Arg Ser Leu
                200   205   210

Gly Asp Arg Pro Thr Leu Arg Thr Val Lys His Asp Ser Lys Trp
                215   220   225

Phe Lys Glu Pro Tyr Phe Val His Ala Val Glu Trp Gly Ser His
                230   235   240

Val Tyr Phe Phe Phe Arg Glu Ile Ala Met Glu Phe Asn Tyr Leu
                245   250   255

Glu Lys Val Val Val Ser Arg Val Ala Arg Val Cys Lys Asn Asp
                260   265   270

Val Gly Gly Ser Pro Arg Val Leu Glu Lys Gln Trp Thr Ser Phe
                275   280   285

Leu Lys Ala Arg Leu Asn Cys Ser Val Pro Gly Asp Ser His Phe
                290   295   300

Tyr Phe Asn Val Leu Gln Ala Val Thr Gly Val Val Ser Leu Gly

28

```
Gly Arg Pro Val Val Leu Ala Val Phe Ser Thr Pro Ser Asn Ser
            320                      325                      330

Ile Pro Gly Ser Ala Val Cys Ala Phe Asp Leu Thr Gln Val Ala
            335                      340                      345

Ala Val Phe Glu Gly Arg Phe Arg Glu Gln Lys Ser Pro Glu Ser
            350                      355                      360

Ile Trp Thr Pro Val Pro Glu Asp Gln Val Pro Arg Pro Arg Pro
            365                      370                      375

Gly Cys Cys Ala Ala Pro Gly Met Gln Tyr Asn Ala Ser Ser Ala
            380                      385                      390

Leu Pro Asp Asp Ile Leu Asn Phe Val Lys Thr His Pro Leu Met
            395                      400                      405

Asp Glu Ala Val Pro Ser Leu Gly His Ala Pro Trp Ile Leu Arg
            410                      415                      420

Thr Leu Met Arg His Gln Leu Thr Arg Val Ala Val Asp Val Gly
            425                      430                      435

Ala Gly Pro Trp Gly Asn Gln Thr Val Val Phe Leu Gly Ser Glu
            440                      445                      450

Ala Gly Thr Val Leu Lys Phe Leu Val Arg Pro Asn Ala Ser Thr
            455                      460                      465

Ser Gly Thr Ser Gly Leu Ser Val Phe Leu Glu Glu Phe Glu Thr
            470                      475                      480

Tyr Arg Pro Asp Arg Cys Gly Arg Pro Gly Gly Gly Glu Thr Gly
            485                      490                      495

Gln Arg Leu Leu Ser Leu Glu Leu Asp Ala Ala Ser Gly Gly Leu
            500                      505                      510

Leu Ala Ala Phe Pro Arg Cys Val Val Arg Val Pro Val Ala Arg
            515                      520                      525

Cys Gln Gln Tyr Ser Gly Cys Met Lys Asn Cys Ile Gly Ser Gln
            530                      535                      540

Asp Pro Tyr Cys Gly Trp Ala Pro Asp Gly Ser Cys Ile Phe Leu
            545                      550                      555

Ser Pro Gly Thr Arg Ala Ala Phe Glu Gln Asp Val Ser Gly Ala
            560                      565                      570

Ser Thr Ser Gly Leu Gly Asp Cys Thr Gly Leu Leu Arg Ala Ser
            575                      580                      585

Leu Ser Glu Asp Arg Ala Gly Leu Val Ser Val Asn Leu Leu Val
            590                      595                      600
```

```
Thr Ser Ser Val Ala Ala Phe Val Val Gly Ala Val Val Ser Gly
            605                 610                     615

Phe Ser Val Gly Trp Phe Val Gly Leu Arg Glu Arg Arg Glu Leu
            620                 625                     630

Ala Arg Arg Lys Asp Lys Glu Ala Ile Leu Ala His Gly Ala Gly
            635                 640                     645

Glu Ala Val Leu Ser Val Ser Arg Leu Gly Glu Arg Arg Ala Gln
            650                 655                     660

Gly Pro Gly Gly Arg Gly Gly Gly Gly Gly Gly Gly Ala Gly Val
            665                 670                     675

Pro Pro Glu Ala Leu Leu Ala Pro Leu Met Gln Asn Gly Trp Ala
            680                 685                     690

Lys Ala Thr Leu Leu Gln Gly Gly Pro His Asp Leu Asp Ser Gly
            695                 700                     705

Leu Leu Pro Thr Pro Glu Gln Thr Pro Leu Pro Gln Lys Arg Leu
            710                 715                     720

Pro Thr Pro His Pro His Pro His Ala Leu Gly Pro Arg Ala Trp
            725                 730                     735

Asp His Gly His Pro Leu Leu Pro Ala Ser Ala Ser Ser Ser Leu
            740                 745                     750

Leu Leu Leu Ala Pro Ala Arg Ala Pro Glu Gln Pro Pro Ala Pro
            755                 760                     765

Gly Glu Pro Thr Pro Asp Gly Arg Leu Tyr Ala Ala Arg Pro Gly
            770                 775                     780

Arg Ala Ser His Gly Asp Phe Pro Leu Thr Pro His Ala Ser Pro
            785                 790                     795

Asp Arg Arg Arg Val Val Ser Ala Pro Thr Gly Pro Leu Asp Pro
            800                 805                     810

Ala Ser Ala Ala Asp Gly Leu Pro Arg Pro Trp Ser Pro Pro Pro
            815                 820                     825

Thr Gly Ser Leu Arg Arg Pro Leu Gly Pro His Ala Pro Pro Ala
            830                 835                     840

Ala Thr Leu Arg Arg Thr His Thr Phe Asn Ser Gly Glu Ala Arg
            845                 850                     855

Pro Gly Asp Arg His Arg Gly Cys His Ala Arg Pro Gly Thr Asp
            860                 865                     870

Leu Ala His Leu Leu Pro Tyr Gly Gly Ala Asp Arg Thr Ala Pro
            875                 880                     885

Pro Val Pro
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30

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<210> 36
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 36
 gaggacctac cggccggaca g 21

<210> 37
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 37
 atacaccccg agtactgctg gcag 24

<210> 38
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 38
 agacagggca gcggctgctg agcttggagc tggacgcagc tt 42

<210> 39
<211> 2014
<212> DNA
<213> Homo Sapien

<400> 39
 agcaactcaa gttcatcatt gtcctgagag agaggagcag cgcggttctc 50

 ggccgggaca gcagaacgcc aggggaccct cacctgggcg cgccggggca 100

 cgggctttga ttgtcctggg gtcgcggaga cccgcgcgcc tgccctgcac 150

 gccgggcggc aacctttgca gtcgcgttgg ctgctgcgat cggccggcgg 200

 gtccctgccg aaggctcggc tgcttctgtc cacctcttac acttcttcat 250

 ttatcggtgg atcatttcga gagtccgtct tgtaaatgtt tggcactttg 300

 ctactttatt gcttctttct ggcgacagtt ccagcactcg ccgagaccgg 350

 cggagaaagg cagctgagcc cggagaagag cgaaatatgg ggacccgggc 400

 taaaagcaga cgtcgtcctt cccgcccgct atttctatat tcaggcagtg 450
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gatacatcag ggaataaatt cacatcttct ccaggcgaaa aggtcttcca 500

ggtgaaagtc tcagcaccag aggagcaatt cactagagtt ggagtccagg 550

tttttagaccg aaaagatggg tccttcatag taagatacag aatgtatgca 600

agctacaaaa atctgaaggt ggaaattaaa ttccaagggc aacatgtggc 650

caaatcccca tatattttaa aagggccggt ttaccatgag aactgtgact 700

gtcctctgca agatagtgca gcctggctac gggagatgaa ctgccctgaa 750

accattgctc agattcagag agatctggca catttccctg ctgtggatcc 800

agaaaagatt gcagtagaaa tcccaaaaag atttggacag aggcagagcc 850

tatgtcacta caccttaaag gataacaagg tttatatcaa gactcatggt 900

gaacatgtag gttttagaat tttcatggat gccatactac tttctttgac 950

tagaaaggtg aagatgccag atgtggagct ctttgttaat ttgggagact 1000

ggcctttgga aaaaaagaaa tccaattcaa acatccatcc gatctttttcc 1050

tggtgtggct ccacagattc caaggatatc gtgatgccta cgtacgattt 1100

gactgattct gttctggaaa ccatgggccg ggtaagtctg gatatgatgt 1150

ccgtgcaagc taacacgggt cctccctggg aaagcaaaaa ttccactgcc 1200

gtctggagag ggcgagacag ccgcaaagag agactcgagc tggttaaact 1250

cagtagaaaa cacccagaac tcatagacgc tgctttcacc aacttttttct 1300

tctttaaaca cgatgaaaac ctgtatggtc ccattgtgaa acatatttca 1350

tttttttgatt tcttcaagca taagtatcaa ataaatatcg atggcactgt 1400

agcagcttat cgcctgccat atttgctagt tggtgacagt gttgtgctga 1450

agcaggattc catctactat gaacatttttt acaatgagct gcagccctgg 1500

aaacactaca ttccagttaa gagcaacctg agcgatctgc tagaaaaact 1550

taaatgggcg aaagatcacg atgaagaggc caaaaagata gcaaaagcag 1600

gacaagaatt tgcaagaaat aatctcatgg gcgatgacat attctgttat 1650

tatttcaaac ttttccagga atatgccaat ttacaagtga gtgagcccca 1700

aatccgagag ggcatgaaaa gggtagaacc acagactgag gacgacctct 1750

tcccttgtac ttgccatagg aaaaagacca agatgaact ctgatatgca 1800

aaataacttc tattagaata atggtgctct gaagactctt cttaactaaa 1850

aagaagaatt tttttaagta ttaattccat ggacaatata aaatctgtgt 1900
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32

gattgtttgc agtatgaaga cacatttcta cttatgcagt attctcatga 1950

ctgtacttta aagtacattt ttagaatttt ataataaaac cacctttatt 2000

ttaaaggaaa aaaa 2014

<210> 40
<211> 502
<212> PRT
<213> Homo Sapien

<400> 40

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Met Phe Gly Thr Leu Leu Leu Tyr Cys Phe Phe Leu Ala Thr Val
  1               5                  10                  15

Pro Ala Leu Ala Glu Thr Gly Gly Glu Arg Gln Leu Ser Pro Glu
                20                  25                  30

Lys Ser Glu Ile Trp Gly Pro Gly Leu Lys Ala Asp Val Val Leu
                35                  40                  45

Pro Ala Arg Tyr Phe Tyr Ile Gln Ala Val Asp Thr Ser Gly Asn
                50                  55                  60

Lys Phe Thr Ser Ser Pro Gly Glu Lys Val Phe Gln Val Lys Val
                65                  70                  75

Ser Ala Pro Glu Glu Gln Phe Thr Arg Val Gly Val Gln Val Leu
                80                  85                  90

Asp Arg Lys Asp Gly Ser Phe Ile Val Arg Tyr Arg Met Tyr Ala
                95                 100                 105

Ser Tyr Lys Asn Leu Lys Val Glu Ile Lys Phe Gln Gly Gln His
               110                 115                 120

Val Ala Lys Ser Pro Tyr Ile Leu Lys Gly Pro Val Tyr His Glu
               125                 130                 135

Asn Cys Asp Cys Pro Leu Gln Asp Ser Ala Ala Trp Leu Arg Glu
               140                 145                 150

Met Asn Cys Pro Glu Thr Ile Ala Gln Ile Gln Arg Asp Leu Ala
               155                 160                 165

His Phe Pro Ala Val Asp Pro Glu Lys Ile Ala Val Glu Ile Pro
               170                 175                 180

Lys Arg Phe Gly Gln Arg Gln Ser Leu Cys His Tyr Thr Leu Lys
               185                 190                 195

Asp Asn Lys Val Tyr Ile Lys Thr His Gly Glu His Val Gly Phe
               200                 205                 210

Arg Ile Phe Met Asp Ala Ile Leu Leu Ser Leu Thr Arg Lys Val
               215                 220                 225

Lys Met Pro Asp Val Glu Leu Phe Val Asn Leu Gly Asp Trp Pro
```

33

Leu Glu Lys Lys Lys Ser Asn Ser Asn Ile His Pro Ile Phe Ser
                    245   250   255

Trp Cys Gly Ser Thr Asp Ser Lys Asp Ile Val Met Pro Thr Tyr
                    260   265   270

Asp Leu Thr Asp Ser Val Leu Glu Thr Met Gly Arg Val Ser Leu
                    275   280   285

Asp Met Met Ser Val Gln Ala Asn Thr Gly Pro Pro Trp Glu Ser
                    290   295   300

Lys Asn Ser Thr Ala Val Trp Arg Gly Arg Asp Ser Arg Lys Glu
                    305   310   315

Arg Leu Glu Leu Val Lys Leu Ser Arg Lys His Pro Glu Leu Ile
                    320   325   330

Asp Ala Ala Phe Thr Asn Phe Phe Phe Phe Lys His Asp Glu Asn
                    335   340   345

Leu Tyr Gly Pro Ile Val Lys His Ile Ser Phe Phe Asp Phe Phe
                    350   355   360

Lys His Lys Tyr Gln Ile Asn Ile Asp Gly Thr Val Ala Ala Tyr
                    365   370   375

Arg Leu Pro Tyr Leu Leu Val Gly Asp Ser Val Val Leu Lys Gln
                    380   385   390

Asp Ser Ile Tyr Tyr Glu His Phe Tyr Asn Glu Leu Gln Pro Trp
                    395   400   405

Lys His Tyr Ile Pro Val Lys Ser Asn Leu Ser Asp Leu Leu Glu
                    410   415   420

Lys Leu Lys Trp Ala Lys Asp His Asp Glu Glu Ala Lys Lys Ile
                    425   430   435

Ala Lys Ala Gly Gln Glu Phe Ala Arg Asn Asn Leu Met Gly Asp
                    440   445   450

Asp Ile Phe Cys Tyr Tyr Phe Lys Leu Phe Gln Glu Tyr Ala Asn
                    455   460   465

Leu Gln Val Ser Glu Pro Gln Ile Arg Glu Gly Met Lys Arg Val
                    470   475   480

Glu Pro Gln Thr Glu Asp Asp Leu Phe Pro Cys Thr Cys His Arg
                    485   490   495

Lys Lys Thr Lys Asp Glu Leu
                    500

<210> 41
<211> 26

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<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 41
 gaaggtggaa attaaattcc aagggc 26

<210> 42
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 42
 cgataagctg ctacagtgcc atcg 24

<210> 43
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 43
 gtgactgtcc tctgcaagat agtgcagcct ggctacggga 40

<210> 44
<211> 2395
<212> DNA
<213> Homo Sapien

<400> 44
 cctggagccg gaagcgcggc tgcagcaggg cgaggctcca ggtggggtcg 50

 gttccgcatc cagcctagcg tgtccacgat gcggctgggc tccgggactt 100

 tcgctacctg ttgcgtagcg atcgaggtgc tagggatcgc ggtcttcctt 150

 cggggattct tcccggctcc cgttcgttcc tctgccagag cggaacacgg 200

 agcggagccc ccagcgcccg aaccctcggc tggagccagt tctaactgga 250

 ccacgctgcc accacctctc ttcagtaaag ttgttattgt tctgatagat 300

 gccttgagag atgattttgt gtttgggtca aagggtgtga aatttatgcc 350

 ctacacaact taccttgtgg aaaaaggagc atctcacagt tttgtggctg 400

 aagcaaagcc acctacagtt actatgcctc gaatcaaggc attgatgacg 450

 gggagccttc ctggctttgt cgacgtcatc aggaacctca attctcctgc 500

 actgctggaa gacagtgtga taagacaagc aaaagcagct ggaaaaagaa 550
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35

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tagtcttttta tggagatgaa acctgggtta aattattccc aaagcatttt 600

gtggaatatg atggaacaac ctcattttttc gtgtcagatt acacagaggt 650

ggataataat gtcacgaggc atttggataa agtattaaaa agaggagatt 700

gggacatatt aatcctccac tacctggggc tggaccacat tggccacatt 750

tcagggccca acagccccct gattgggcag aagctgagcg agatggacag 800

cgtgctgatg aagatccaca cctcactgca gtcgaaggag agagagacgc 850

ctttacccaa tttgctggtt ctttgtggtg accatggcat gtctgaaaca 900

ggaagtcacg gggcctcctc caccgaggag gtgaatacac ctctgatttt 950

aatcagttct gcgtttgaaa ggaaacccgg tgatatccga catccaaagc 1000

acgtccaata gacggatgtg gctgcgacac tggcgatagc acttggctta 1050

ccgattccaa aagacagtgt agggagcctc ctattcccag ttgtggaagg 1100

aagaccaatg agagagcagt tgagattttt acatttgaat acagtgcagc 1150

ttagtaaact gttgcaagag aatgtgccgt catatgaaaa agatcctggg 1200

tttgagcagt ttaaaatgtc agaaagattg catgggaact ggatcagact 1250

gtacttggag gaaaagcatt cagaagtcct attcaacctg ggctccaagg 1300

ttctcaggca gtacctggat gctctgaaga cgctgagctt gtccctgagt 1350

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tctgctcttt tatttggtga tcctggttct ttcggccgtt cacgtcattg 1500

tgtgcacctc agctgaaagt tcgtgctact tctgtggcct ctcgtggctg 1550

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gccaagtgct ggcagtgccc tggacagggg gcctcaggga aggacgtgga 1650

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cagctgaggg ggtgtgtgaa tcggacagcc tcccagcaga ggtgtgggag 1850

ctgcagctga gggaagaaga gacaatcggc ctggacactc aggagggtca 1900

aaaggagact tggtcgcacc actcatcctg ccacccccag aatgcatcct 1950

gcctcatcag gtccagattt ctttccaagg cggacgtttt ctgttggaat 2000
```

36

tcttagtcct tggcctcgga caccttcatt cgttagctgg ggagtggtgg 2050

tgaggcagtg aagaagaggc ggatggtcac actcagatcc acagagccca 2100

ggatcaaggg acccactgca gtggcagcag gactgttggg cccccacccc 2150

aaccctgcac agccctcatc ccctcttggc ttgagccgtc agaggccctg 2200

tgctgagtgt ctgaccgaga cactcacagc tttgtcatca gggcacaggc 2250

ttcctcggag ccaggatgat ctgtgccacg cttgcacctc gggcccatct 2300

gggctcatgc tctctctcct gctattgaat tagtacctag ctgcacacag 2350

tatgtagtta ccaaaagaat aaacggcaat aattgagaaa aaaaa 2395

<210> 45
<211> 310
<212> PRT
<213> Homo Sapien

<400> 45

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Met Arg Leu Gly Ser Gly Thr Phe Ala Thr Cys Cys Val Ala Ile
 1               5                  10                  15

Glu Val Leu Gly Ile Ala Val Phe Leu Arg Gly Phe Phe Pro Ala
                20                  25                  30

Pro Val Arg Ser Ser Ala Arg Ala Glu His Gly Ala Glu Pro Pro
                35                  40                  45

Ala Pro Glu Pro Ser Ala Gly Ala Ser Ser Asn Trp Thr Thr Leu
                50                  55                  60

Pro Pro Pro Leu Phe Ser Lys Val Val Ile Val Leu Ile Asp Ala
                65                  70                  75

Leu Arg Asp Asp Phe Val Phe Gly Ser Lys Gly Val Lys Phe Met
                80                  85                  90

Pro Tyr Thr Thr Tyr Leu Val Glu Lys Gly Ala Ser His Ser Phe
                95                  100                 105

Val Ala Glu Ala Lys Pro Pro Thr Val Thr Met Pro Arg Ile Lys
                110                 115                 120

Ala Leu Met Thr Gly Ser Leu Pro Gly Phe Val Asp Val Ile Arg
                125                 130                 135

Asn Leu Asn Ser Pro Ala Leu Leu Glu Asp Ser Val Ile Arg Gln
                140                 145                 150

Ala Lys Ala Ala Gly Lys Arg Ile Val Phe Tyr Gly Asp Glu Thr
                155                 160                 165

Trp Val Lys Leu Phe Pro Lys His Phe Val Glu Tyr Asp Gly Thr
                170                 175                 180
```

37

```
Thr Ser Phe Phe Val Ser Asp Tyr Thr Glu Val Asp Asn Asn Val
            185                 190                 195

Thr Arg His Leu Asp Lys Val Leu Lys Arg Gly Asp Trp Asp Ile
            200                 205                 210

Leu Ile Leu His Tyr Leu Gly Leu Asp His Ile Gly His Ile Ser
            215                 220                 225

Gly Pro Asn Ser Pro Leu Ile Gly Gln Lys Leu Ser Glu Met Asp
            230                 235                 240

Ser Val Leu Met Lys Ile His Thr Ser Leu Gln Ser Lys Glu Arg
            245                 250                 255

Glu Thr Pro Leu Pro Asn Leu Leu Val Leu Cys Gly Asp His Gly
            260                 265                 270

Met Ser Glu Thr Gly Ser His Gly Ala Ser Ser Thr Glu Glu Val
            275                 280                 285

Asn Thr Pro Leu Ile Leu Ile Ser Ser Ala Phe Glu Arg Lys Pro
            290                 295                 300

Gly Asp Ile Arg His Pro Lys His Val Gln
            305                 310
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<210> 46
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 46
 cgggactttc gctacctgtt gc 22

<210> 47
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 47
 catcatattc cacaaaatgc tttggg 26

<210> 48
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 48

ccttcggggga ttcttcccgg ctcccgttcg ttcctctg 38

<210> 49
<211> 918
<212> DNA
<213> Homo Sapien

<400> 49
agccaggcag cacatcacag cgggaggagc tgtcccaggt ggcccagctc 50

agcaatggca atggggggtcc ccagagtcat tctgctctgc ctctttgggg 100

ctgcgctctg cctgacaggg tcccaagccc tgcagtgcta cagctttgag 150

cacacctact ttggcccctt tgacctcagg gccatgaagc tgcccagcat 200

ctcctgtcct catgagtgct ttgaggctat cctgtctctg gacaccgggt 250

atcgcgcgcc ggtgaccctg gtgcggaagg gctgctggac cgggcctcct 300

gcgggccaga cgcaatcgaa cccggacgcg ctgccgccag actactcggt 350

ggtgcgcggc tgcacaactg acaaatgcaa cgcccacctc atgactcatg 400

acgccctccc caacctgagc caagcacccg acccgccgac gctcagcggc 450

gccgagtgct acgcctgtat cggggtccac caggatgact cgctatcgg 500

caggtcccga cgagtccagt gtcaccagga ccagaccgcc tgcttccagg 550

gcagtggcag aatgacagtt ggcaatttct cagtccctgt gtacatcaga 600

acctgccacc ggccctcctg caccaccgag ggcaccacca gcccctggac 650

agccatcgac ctccagggct cctgctgtga ggggtacctc tgcaacagga 700

aatccatgac ccagcccttc accagtgctt cagccaccac ccctcccga 750

gcactacagg tcctggccct gctcctccca gtcctcctgc tggtggggct 800

ctcagcatag accgcccctc caggatgctg gggacagggc tcacacacct 850

cattcttgct gcttcagccc ctatcacata gctcactgga aaatgatgtt 900

aaagtaagaa ttgcaaaa 918

<210> 50
<211> 251
<212> PRT
<213> Homo Sapien

<400> 50
Met Ala Met Gly Val Pro Arg Val Ile Leu Leu Cys Leu Phe Gly
1   5   10   15

Ala Ala Leu Cys Leu Thr Gly Ser Gln Ala Leu Gln Cys Tyr Ser
                20   25   30

39

```
Phe Glu His Thr Tyr Phe Gly Pro Phe Asp Leu Arg Ala Met Lys
            35                      40                      45

Leu Pro Ser Ile Ser Cys Pro His Glu Cys Phe Glu Ala Ile Leu
            50                      55                      60

Ser Leu Asp Thr Gly Tyr Arg Ala Pro Val Thr Leu Val Arg Lys
            65                      70                      75

Gly Cys Trp Thr Gly Pro Pro Ala Gly Gln Thr Gln Ser Asn Pro
            80                      85                      90

Asp Ala Leu Pro Pro Asp Tyr Ser Val Val Arg Gly Cys Thr Thr
            95                      100                     105

Asp Lys Cys Asn Ala His Leu Met Thr His Asp Ala Leu Pro Asn
            110                     115                     120

Leu Ser Gln Ala Pro Asp Pro Pro Thr Leu Ser Gly Ala Glu Cys
            125                     130                     135

Tyr Ala Cys Ile Gly Val His Gln Asp Asp Cys Ala Ile Gly Arg
            140                     145                     150

Ser Arg Arg Val Gln Cys His Gln Asp Gln Thr Ala Cys Phe Gln
            155                     160                     165

Gly Ser Gly Arg Met Thr Val Gly Asn Phe Ser Val Pro Val Tyr
            170                     175                     180

Ile Arg Thr Cys His Arg Pro Ser Cys Thr Thr Glu Gly Thr Thr
            185                     190                     195

Ser Pro Trp Thr Ala Ile Asp Leu Gln Gly Ser Cys Cys Glu Gly
            200                     205                     210

Tyr Leu Cys Asn Arg Lys Ser Met Thr Gln Pro Phe Thr Ser Ala
            215                     220                     225

Ser Ala Thr Thr Pro Pro Arg Ala Leu Gln Val Leu Ala Leu Leu
            230                     235                     240

Leu Pro Val Leu Leu Leu Val Gly Leu Ser Ala
            245                     250
```

<210> 51
<211> 3288
<212> DNA
<213> Homo Sapien

<400> 51
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 gattgggaaa gggaaaggac aaaaaagacc cctgggctac acggcgtagg 100

 tgcagggttt cctactgctg ttcttttatg ctgggagctg tggctgtaac 150

 caactaggaa ataacgtatg cagcagctat ggctgtcaga gagttgtgct 200

```
tcccaagaca aaggcaagtc ctgtttcttt ttcttttttg gggagtgtcc 250

ttggcaggtt ctgggtttgg acgttattcg gtgactgagg aaacagagaa 300

aggatccttt gtggtcaatc tggcaaagga tctgggacta gcagaggggg 350

agctggctgc aagggaacc agggtggttt ccgatgataa caaacaatac 400

ctgctcctgg attcacatac cgggaatttg ctcacaaatg agaaactgga 450

ccgagagaag ctgtgtggcc ctaaagagcc ctgtatgctg tatttccaaa 500

ttttaatgga tgatcccttt cagatttacc gggctgagct gagagtcagg 550

gatataaatg atcacgcgcc agtatttcag gacaaagaaa cagtcttaaa 600

aatatcagaa aatacagctg aagggacagc atttagacta gaaagagcac 650

aggatccaga tggaggactt aacggtatcc aaaactacac gatcagcccc 700

aactcttttt tccatattaa cattagtggc ggtgatgaag gcatgatata 750

tccagagcta gtgttggaca aagcactgga tcgggaggag cagggagagc 800

tcagcttaac cctcacagcg ctggatggtg ggtctccatc caggtctggg 850

acctctactg tacgcatcgt tgtcttggac gtcaatgaca atgccccaca 900

gtttgcccag gctctgtatg agacccaggc tccagaaaac agccccattg 950

ggttccttat tgttaaggta tgggcagaag atgtagactc tggagtcaac 1000

gcggaagtat cctattcatt ttttgatgcc tcagaaaata ttcgaacgac 1050

ctttcaaatc aatcctttt ctggggaaat ctttctcaga gaattgcttg 1100

attatgagtt agtaaattct tacaaaataa atatacaggc aatggacggt 1150

ggaggccttt ctgcaagatg tagggtttta gtggaagtat tggacaccaa 1200

tgacaatccc cctgaactga tcgtatcatc attttccaac tctgttgctg 1250

agaattctcc tgagacgccg ctggctgttt ttaagattaa tgacagagac 1300

tctggagaaa atggaaagat ggtttgctac attcaagaga atctgccatt 1350

cctactaaaa ccttctgtgg agaatttta catcctaatt acagaaggcg 1400

cgctggacag agagatcaga gccgagtaca acatcactat caccgtcact 1450

gacttgggga cacccaggct gaaaaccgag cacaacataa cggtcctggt 1500

ctccgacgtc aatgacaacg cccccgcctt cacccaaacc tcctacaccc 1550

tgttcgtccg cgagaacaac agccccgccc tgcacatcgg cagcgtcagc 1600

gccacagaca gagactcggg caccaacgcc caggtcacct actcgctgct 1650
```

```
gccgccccaa gacccgcacc tgcccctcgc ctccctggtc tccatcaacg 1700

cggacaacgg ccacctgttc gccctcaggt cgctggacta cgaggccctg 1750

caggctttcg agttccgcgt gggcgccaca gaccgcggct cccccgcgct 1800

gagcagagag gcgctggtgc gcgtgctggt gctggacgcc aacgacaact 1850

cgcccttcgt gctgtacccg ctgcagaacg gctccgcgcc ctgcaccgag 1900

ctggtgcccc gggcggccga gccgggctac ctggtgacca aggtggtggc 1950

ggtggacggc gactcgggcc agaacgcctg gctgtcgtac cagctgctca 2000

aggccacgga gcccgggctg ttcggtgtgt gggcgcacaa tggggaggtg 2050

cgcaccgcca ggctgctgag cgagcgcgac gcagccaagc acaggctcgt 2100

ggtgcttgtc aaggacaatg gcgagcctcc tcgctcggcc accgccacgc 2150

tgcacttgct cctggtggac ggcttctccc agccctacct gcctctcccg 2200

gaggcggccc cggcccaggc ccaggccgag gccgacttgc tcaccgtcta 2250

cctggtggtg gcgttggcct cggtgtcttc gctcttcctc ctctcggtgc 2300

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gatattcagg cacagggccc tgggaggaag ggtgaagaaa attccacctt 2550

ccgaaatagc tttggattta atattcagta aagtctgttt ttagtttcat 2600

atacttttgg tgtgttacat agccatgttt ctattagttt acttttaaat 2650

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cccctgtggt tttacaatgt ttcatcattt ttttgcatta ataacaactg 2750

ggtttaattt aatgagtatt tttttctaaa tgatagtgtt aaggttttaa 2800

ttctttccaa ctgcccaagg aattaattac tattatatct cattacagaa 2850

atctgaggtt ttgattcatt tcagagcttg catctcatga ttctaatcac 2900

ttctgtctat agtgtacttg ctctatttaa gaaggcatat ctacatttcc 2950

aaactcattc taacattcta tatattcgtg tttgaaaacc atgtcattta 3000

tttctacatc atgtatttaa aaagaaatat ttctctacta ctatgctcat 3050

gacaaaatga aacaaagcat attgtgagca atactgaaca tcaataatac 3100
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42

cttagttta tatacttatt attttatctt taagcatgct actttttactt 3150

ggccaatatt ttcttatgtt aactttttgct gatgtataaa acagactatg 3200

ccttataatt gaaataaaat tataatctgc ctgaaaatga ataaaaataa 3250

aacattttga aatgtgaaaa aaaaaaaaaa aaaaaaaa 3288

<210> 52
<211> 800
<212> PRT
<213> Homo Sapien

<400> 52
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Met Ala Val Arg Glu Leu Cys Phe Pro Arg Gln Arg Gln Val Leu
 1               5                  10                  15

Phe Leu Phe Leu Phe Trp Gly Val Ser Leu Ala Gly Ser Gly Phe
                20                  25                  30

Gly Arg Tyr Ser Val Thr Glu Glu Thr Glu Lys Gly Ser Phe Val
                35                  40                  45

Val Asn Leu Ala Lys Asp Leu Gly Leu Ala Glu Gly Glu Leu Ala
                50                  55                  60

Ala Arg Gly Thr Arg Val Val Ser Asp Asp Asn Lys Gln Tyr Leu
                65                  70                  75

Leu Leu Asp Ser His Thr Gly Asn Leu Leu Thr Asn Glu Lys Leu
                80                  85                  90

Asp Arg Glu Lys Leu Cys Gly Pro Lys Glu Pro Cys Met Leu Tyr
                95                  100                 105

Phe Gln Ile Leu Met Asp Asp Pro Phe Gln Ile Tyr Arg Ala Glu
                110                 115                 120

Leu Arg Val Arg Asp Ile Asn Asp His Ala Pro Val Phe Gln Asp
                125                 130                 135

Lys Glu Thr Val Leu Lys Ile Ser Glu Asn Thr Ala Glu Gly Thr
                140                 145                 150

Ala Phe Arg Leu Glu Arg Ala Gln Asp Pro Asp Gly Gly Leu Asn
                155                 160                 165

Gly Ile Gln Asn Tyr Thr Ile Ser Pro Asn Ser Phe Phe His Ile
                170                 175                 180

Asn Ile Ser Gly Gly Asp Glu Gly Met Ile Tyr Pro Glu Leu Val
                185                 190                 195

Leu Asp Lys Ala Leu Asp Arg Glu Glu Gln Gly Glu Leu Ser Leu
                200                 205                 210

Thr Leu Thr Ala Leu Asp Gly Gly Ser Pro Ser Arg Ser Gly Thr
                215                 220                 225
```

43

```
Ser Thr Val Arg Ile Val Val Leu Asp Val Asn Asp Asn Ala Pro
              230             235                 240

Gln Phe Ala Gln Ala Leu Tyr Glu Thr Gln Ala Pro Glu Asn Ser
              245             250                 255

Pro Ile Gly Phe Leu Ile Val Lys Val Trp Ala Glu Asp Val Asp
              260             265                 270

Ser Gly Val Asn Ala Glu Val Ser Tyr Ser Phe Phe Asp Ala Ser
              275             280                 285

Glu Asn Ile Arg Thr Thr Phe Gln Ile Asn Pro Phe Ser Gly Glu
              290             295                 300

Ile Phe Leu Arg Glu Leu Leu Asp Tyr Glu Leu Val Asn Ser Tyr
              305             310                 315

Lys Ile Asn Ile Gln Ala Met Asp Gly Gly Gly Leu Ser Ala Arg
              320             325                 330

Cys Arg Val Leu Val Glu Val Leu Asp Thr Asn Asp Asn Pro Pro
              335             340                 345

Glu Leu Ile Val Ser Ser Phe Ser Asn Ser Val Ala Glu Asn Ser
              350             355                 360

Pro Glu Thr Pro Leu Ala Val Phe Lys Ile Asn Asp Arg Asp Ser
              365             370                 375

Gly Glu Asn Gly Lys Met Val Cys Tyr Ile Gln Glu Asn Leu Pro
              380             385                 390

Phe Leu Leu Lys Pro Ser Val Glu Asn Phe Tyr Ile Leu Ile Thr
              395             400                 405

Glu Gly Ala Leu Asp Arg Glu Ile Arg Ala Glu Tyr Asn Ile Thr
              410             415                 420

Ile Thr Val Thr Asp Leu Gly Thr Pro Arg Leu Lys Thr Glu His
              425             430                 435

Asn Ile Thr Val Leu Val Ser Asp Val Asn Asp Asn Ala Pro Ala
              440             445                 450

Phe Thr Gln Thr Ser Tyr Thr Leu Phe Val Arg Glu Asn Asn Ser
              455             460                 465

Pro Ala Leu His Ile Gly Ser Val Ser Ala Thr Asp Arg Asp Ser
              470             475                 480

Gly Thr Asn Ala Gln Val Thr Tyr Ser Leu Leu Pro Pro Gln Asp
              485             490                 495

Pro His Leu Pro Leu Ala Ser Leu Val Ser Ile Asn Ala Asp Asn
              500             505                 510

Gly His Leu Phe Ala Leu Arg Ser Leu Asp Tyr Glu Ala Leu Gln
```

44

```
              515                    520                    525
Ala Phe Glu Phe Arg Val Gly Ala Thr Asp Arg Gly Ser Pro Ala
                530                    535                    540

Leu Ser Arg Glu Ala Leu Val Arg Val Leu Val Leu Asp Ala Asn
                545                    550                    555

Asp Asn Ser Pro Phe Val Leu Tyr Pro Leu Gln Asn Gly Ser Ala
                560                    565                    570

Pro Cys Thr Glu Leu Val Pro Arg Ala Ala Glu Pro Gly Tyr Leu
                575                    580                    585

Val Thr Lys Val Val Ala Val Asp Gly Asp Ser Gly Gln Asn Ala
                590                    595                    600

Trp Leu Ser Tyr Gln Leu Leu Lys Ala Thr Glu Pro Gly Leu Phe
                605                    610                    615

Gly Val Trp Ala His Asn Gly Glu Val Arg Thr Ala Arg Leu Leu
                620                    625                    630

Ser Glu Arg Asp Ala Ala Lys His Arg Leu Val Val Leu Val Lys
                635                    640                    645

Asp Asn Gly Glu Pro Pro Arg Ser Ala Thr Ala Thr Leu His Leu
                650                    655                    660

Leu Leu Val Asp Gly Phe Ser Gln Pro Tyr Leu Pro Leu Pro Glu
                665                    670                    675

Ala Ala Pro Ala Gln Ala Gln Ala Glu Ala Asp Leu Leu Thr Val
                680                    685                    690

Tyr Leu Val Val Ala Leu Ala Ser Val Ser Ser Leu Phe Leu Leu
                695                    700                    705

Ser Val Leu Leu Phe Val Ala Val Arg Leu Cys Arg Arg Ser Arg
                710                    715                    720

Ala Ala Ser Val Gly Arg Cys Ser Val Pro Glu Gly Pro Phe Pro
                725                    730                    735

Gly His Leu Val Asp Val Arg Gly Ala Glu Thr Leu Ser Gln Ser
                740                    745                    750

Tyr Gln Tyr Glu Val Cys Leu Thr Gly Gly Pro Gly Thr Ser Glu
                755                    760                    765

Phe Lys Phe Leu Lys Pro Val Ile Ser Asp Ile Gln Ala Gln Gly
                770                    775                    780

Pro Gly Arg Lys Gly Glu Glu Asn Ser Thr Phe Arg Asn Ser Phe
                785                    790                    795

Gly Phe Asn Ile Gln
                800
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45

<210> 53
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 53
 ctggggagtg tccttggcag gttc 24

<210> 54
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 54
 cagcatacag ggctctttag ggcacac 27

<210> 55
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 55
 cggtgactga ggaaacagag aaaggatcct ttgtggtcaa tctggc 46

<210> 56
<211> 2242
<212> DNA
<213> Homo Sapien

<220>
<221> unsure
<222> 2181
<223> unknown base

<400> 56
 gaatgaatac ctccgaagcc gctttgttct ccagatgtga atagctccac 50

 tataccagcc tcgtcttcct tccgggggac aacgtgggtc agggcacaga 100

 gagatattta atgtcaccct cttggggctt tcatgggact ccctctgcca 150

 cattttttgg aggttgggaa agttgctaga ggcttcagaa ctccagccta 200

 atggatccca aactcgggag aatggctgcg tccctgctgg ctgtgctgct 250

 gctgctgctg gagcgcggca tgttctcctc accctccccg ccccggcgc 300

 tgttagagaa agtcttccag tacattgacc tccatcagga tgaatttgtg 350

46

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cagacgctga aggagtgggt ggccatcgag agcgactctg tccagcctgt  400

gcctcgcttc agacaagagc tcttcagaat gatggccgtg gctgcggaca  450

cgctgcagcg cctgggggcc cgtgtggcct cggtggacat gggtcctcag  500

cagctgcccg atggtcagag tcttccaata cctcccgtca tcctggccga  550

actggggagc gatcccacga aaggcaccgt gtgcttctac ggccacttgg  600

acgtgcagcc tgctgaccgg ggcgatgggt ggctcacgga cccctatgtg  650

ctgacggagg tagacgggaa actttatgga cgaggagcga ccgacaacaa  700

aggccctgtc ttggcttgga tcaatgctgt gagcgccttc agagccctgg  750

agcaagatct tcctgtgaat atcaaattca tcattgaggg gatggaagag  800

gctggctctg ttgccctgga ggaacttgtg gaaaagaaa aggaccgatt  850

cttctctggt gtggactaca ttgtaatttc agataacctg tggatcagcc  900

aaaggaagcc agcaatcact tatggaaccc gggggaacag ctacttcatg  950

gtggaggtga atgcagaga ccaggatttt cactcaggaa cctttggtgg 1000

catccttcat gaaccaatgg ctgatctggt tgctcttctc ggtagcctgg 1050

tagactcgtc tggtcatatc ctggtccctg gaatctatga tgaagtggtt 1100

cctcttacag aagaggaaat aaatacatac aaagccatcc atctagacct 1150

agaagaatac cggaatagca gccgggttga gaaatttctg ttcgatacta 1200

aggaggagat tctaatgcac ctctggaggt acccatctct ttctattcat 1250

gggatcgagg gcgcgtttga tgagcctgga actaaaacag tcatacctgg 1300

ccgagttata ggaaaatttt caatccgtct agtccctcac atgaatgtgt 1350

ctgcggtgga aaaacaggtg acacgacatc ttgaagatgt gttctccaaa 1400

agaaatagtt ccaacaagat ggttgtttcc atgactctag gactacaccc 1450

gtggattgca aatattgatg acacccagta tctcgcagca aaaagagcga 1500

tcagaacagt gtttggaaca gaaccagata tgatccggga tggatccacc 1550

attccaattg ccaaaatgtt ccaggagatc gtccacaaga gcgtggtgct 1600

aattccgctg ggagctgttg atgatggaga acattcgcag aatgagaaaa 1650

tcaacaggtg gaactacata gagggaacca aattatttgc tgccttttc 1700

ttagagatgg cccagctcca ttaatcacaa gaaccttcta gtctgatctg 1750

atccactgac agattcacct cccccacatc cctagacagg gatggaatgt 1800
```

47

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aaatatccag agaatttggg tctagtatag tacattttcc cttccattta 1850

aaatgtcttg ggatatctgg atcagtaata aaatatttca aaggcacaga 1900

tgttggaaat ggtttaaggt cccccactgc acaccttcct caagtcatag 1950

ctgcttgcag caacttgatt tccccaagtc ctgtgcaata gccccaggat 2000

tggattcctt ccaacctttt agcatatctc caaccttgca atttgattgg 2050

cataatcact ccggtttgct ttctaggtcc tcaagtgctc gtgacacata 2100

atcattccat ccaatgatcg cctttgcttt accactcttt ccttttatct 2150

tattaataaa aatgttggtc tccaccactg nctcccaaaa aaaaaaaaaa 2200

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aa 2242
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<210> 57
<211> 507
<212> PRT
<213> Homo Sapien

<400> 57

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Met Asp Pro Lys Leu Gly Arg Met Ala Ala Ser Leu Leu Ala Val
 1               5                  10                   15

Leu Leu Leu Leu Leu Glu Arg Gly Met Phe Ser Ser Pro Ser Pro
                20                  25                   30

Pro Pro Ala Leu Leu Glu Lys Val Phe Gln Tyr Ile Asp Leu His
                35                  40                   45

Gln Asp Glu Phe Val Gln Thr Leu Lys Glu Trp Val Ala Ile Glu
                50                  55                   60

Ser Asp Ser Val Gln Pro Val Pro Arg Phe Arg Gln Glu Leu Phe
                65                  70                   75

Arg Met Met Ala Val Ala Ala Asp Thr Leu Gln Arg Leu Gly Ala
                80                  85                   90

Arg Val Ala Ser Val Asp Met Gly Pro Gln Gln Leu Pro Asp Gly
                95                  100                  105

Gln Ser Leu Pro Ile Pro Pro Val Ile Leu Ala Glu Leu Gly Ser
                110                 115                  120

Asp Pro Thr Lys Gly Thr Val Cys Phe Tyr Gly His Leu Asp Val
                125                 130                  135

Gln Pro Ala Asp Arg Gly Asp Gly Trp Leu Thr Asp Pro Tyr Val
                140                 145                  150

Leu Thr Glu Val Asp Gly Lys Leu Tyr Gly Arg Gly Ala Thr Asp
                155                 160                  165

Asn Lys Gly Pro Val Leu Ala Trp Ile Asn Ala Val Ser Ala Phe
```

48
```

```
                    170                    175                    180
Arg Ala Leu Glu Gln Asp Leu Pro Val Asn Ile Lys Phe Ile Ile
                185                    190                    195

Glu Gly Met Glu Glu Ala Gly Ser Val Ala Leu Glu Glu Leu Val
                200                    205                    210

Glu Lys Glu Lys Asp Arg Phe Phe Ser Gly Val Asp Tyr Ile Val
                215                    220                    225

Ile Ser Asp Asn Leu Trp Ile Ser Gln Arg Lys Pro Ala Ile Thr
                230                    235                    240

Tyr Gly Thr Arg Gly Asn Ser Tyr Phe Met Val Glu Val Lys Cys
                245                    250                    255

Arg Asp Gln Asp Phe His Ser Gly Thr Phe Gly Gly Ile Leu His
                260                    265                    270

Glu Pro Met Ala Asp Leu Val Ala Leu Leu Gly Ser Leu Val Asp
                275                    280                    285

Ser Ser Gly His Ile Leu Val Pro Gly Ile Tyr Asp Glu Val Val
                290                    295                    300

Pro Leu Thr Glu Glu Glu Ile Asn Thr Tyr Lys Ala Ile His Leu
                305                    310                    315

Asp Leu Glu Glu Tyr Arg Asn Ser Ser Arg Val Glu Lys Phe Leu
                320                    325                    330

Phe Asp Thr Lys Glu Glu Ile Leu Met His Leu Trp Arg Tyr Pro
                335                    340                    345

Ser Leu Ser Ile His Gly Ile Glu Gly Ala Phe Asp Glu Pro Gly
                350                    355                    360

Thr Lys Thr Val Ile Pro Gly Arg Val Ile Gly Lys Phe Ser Ile
                365                    370                    375

Arg Leu Val Pro His Met Asn Val Ser Ala Val Glu Lys Gln Val
                380                    385                    390

Thr Arg His Leu Glu Asp Val Phe Ser Lys Arg Asn Ser Ser Asn
                395                    400                    405

Lys Met Val Val Ser Met Thr Leu Gly Leu His Pro Trp Ile Ala
                410                    415                    420

Asn Ile Asp Asp Thr Gln Tyr Leu Ala Ala Lys Arg Ala Ile Arg
                425                    430                    435

Thr Val Phe Gly Thr Glu Pro Asp Met Ile Arg Asp Gly Ser Thr
                440                    445                    450

Ile Pro Ile Ala Lys Met Phe Gln Glu Ile Val His Lys Ser Val
                455                    460                    465
```

49

Val Leu Ile Pro Leu Gly Ala Val Asp Asp Gly Glu His Ser Gln
          470   475   480

Asn Glu Lys Ile Asn Arg Trp Asn Tyr Ile Glu Gly Thr Lys Leu
          485   490   495

Phe Ala Ala Phe Phe Leu Glu Met Ala Gln Leu His
          500   505

<210> 58
<211> 1470
<212> DNA
<213> Homo Sapien

<400> 58
ctcggctgga tttaaggttg ccgctagccg cctgggaatt taagggaccc 50

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ctttgtcatg ggacctgtgc ggttgggaat attgcttttc ctttttttgg 150

ccgtgcacga ggcttgggct gggatgttga aggaggagga cgatgacaca 200

gaacgcttgc ccagcaaatg cgaagtgtgt aagctgctga gcacagagct 250

acaggcggaa ctgagtcgca ccggtcgatc tcgagaggtg ctggagctgg 300

ggcaggtgct ggatacaggc aagaggaaga gacacgtgcc ttacagcgtt 350

tcagagacaa ggctggaaga ggccttagag aatttatgtg agcggatcct 400

ggactatagt gttcacgctg agcgcaaggg ctcactgaga tatgccaagg 450

gtcagagtca gaccatggca cactgaaag gcctagtgca gaagggggtg 500

aaggtggatc tggggatccc tctggagctt tgggatgagc ccagcgtgga 550

ggtcacatac ctcaagaagc agtgtgagac catgttggag gagtttgaag 600

acattgtggg agactggtac ttccaccatc aggagcagcc cctacaaaat 650

tttctctgtg aaggtcatgt gctcccagct gctgaaactg catgtctaca 700

ggaaacttgg actggaaagg agatcacaga tggggaagag aaaacagaag 750

gggaggaaga gcaggaggag gaggaggaag aggaggaaga ggaagggggа 800

gacaagatga ccaagacagg aagccacccc aaacttgacc gagaagatct 850

ttgacccttg cctttgagcc cccaggaggg aagggatca tggagagccc 900

tctaaagcct gcactctccc tgctccacag ctttcagggt gtgtttatga 950

gtgactccac ccaagcttgt agctgttctc tccatctaa cctcaggcaa 1000

gatcctggtg aaacagcatg acatggcttc tggggtggag ggtgggggtg 1050

gaggtcctgc tcctagagat gaactctatc cagccccta attggcaggt 1100

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gtatgtgctg acagtactga aagctttcct ctttaactga tcccacccccc 1150

acccaaaagt cagcagtggc actggagctg tgggctttgg ggaagtcact 1200

tagctcctta aggtctgttt ttagacccctt ccaaggaaga ggccagaacg 1250

gacattctct gcgatctata tacattgcct gtatccagga ggctacacac 1300

cagcaaaccg tgaaggagaa tgggacactg ggtcatggcc tggagttgct 1350

gataatttag gtgggataga tacttggtct acttaagctc aatgtaaccc 1400

agagcccacc atatagtttt ataggtgctc aactttctat atcgctatta 1450

aacttttttc tttttttcta 1470
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<210> 59
<211> 248
<212> PRT
<213> Homo Sapien

<400> 59

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Met Gly Pro Val Arg Leu Gly Ile Leu Leu Phe Leu Phe Leu Ala
 1               5                  10                  15

Val His Glu Ala Trp Ala Gly Met Leu Lys Glu Glu Asp Asp Asp
                20                  25                  30

Thr Glu Arg Leu Pro Ser Lys Cys Glu Val Cys Lys Leu Leu Ser
                35                  40                  45

Thr Glu Leu Gln Ala Glu Leu Ser Arg Thr Gly Arg Ser Arg Glu
                50                  55                  60

Val Leu Glu Leu Gly Gln Val Leu Asp Thr Gly Lys Arg Lys Arg
                65                  70                  75

His Val Pro Tyr Ser Val Ser Glu Thr Arg Leu Glu Glu Ala Leu
                80                  85                  90

Glu Asn Leu Cys Glu Arg Ile Leu Asp Tyr Ser Val His Ala Glu
                95                  100                 105

Arg Lys Gly Ser Leu Arg Tyr Ala Lys Gly Gln Ser Gln Thr Met
                110                 115                 120

Ala Thr Leu Lys Gly Leu Val Gln Lys Gly Val Lys Val Asp Leu
                125                 130                 135

Gly Ile Pro Leu Glu Leu Trp Asp Glu Pro Ser Val Glu Val Thr
                140                 145                 150

Tyr Leu Lys Lys Gln Cys Glu Thr Met Leu Glu Glu Phe Glu Asp
                155                 160                 165

Ile Val Gly Asp Trp Tyr Phe His His Gln Glu Gln Pro Leu Gln
                170                 175                 180
```

51

```
Asn Phe Leu Cys Glu Gly His Val Leu Pro Ala Ala Glu Thr Ala
            185                 190                 195

Cys Leu Gln Glu Thr Trp Thr Gly Lys Glu Ile Thr Asp Gly Glu
            200                 205                 210

Glu Lys Thr Glu Gly Glu Glu Glu Gln Glu Glu Glu Glu Glu Glu
            215                 220                 225

Glu Glu Glu Glu Gly Gly Asp Lys Met Thr Lys Thr Gly Ser His
            230                 235                 240

Pro Lys Leu Asp Arg Glu Asp Leu
            245
```

<210> 60
<211> 890
<212> DNA
<213> Homo Sapien

<400> 60
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aagtacttgt gtccgggtgg tggactggat tagctgcgga gccctggaag 50

ctgcctgtcc ttctccctgt gcttaaccag aggtgcccat gggttggaca 100

atgaggctgg tcacagcagc actgttactg ggtctcatga tggtggtcac 150

tggagacgag gatgagaaca gcccgtgtgc ccatgaggcc ctcttggacg 200

aggacaccct cttttgccag ggccttgaag ttttctaccc agagttgggg 250

aacattggct gcaaggttgt tcctgattgt aacaactaca gacagaagat 300

cacctcctgg atggagccga tagtcaagtt cccggggggc gtggacggcg 350

caacctatat cctggtgatg gtggatccag atgcccctag cagagcagaa 400

cccagacaga gattctggag acattggctg gtaacagata tcaagggcgc 450

cgacctgaag aaagggaaga ttcagggcca ggagttatca gcctaccagg 500

ctccctcccc accggcacac agtggcttcc atcgctacca gttctttgtc 550

tatcttcagg aaggaaaagt catctctctc cttcccaagg aaaacaaaac 600

tcgaggctct tggaaaatgg acagatttct gaaccgcttc cacctgggcg 650

aacctgaagc aagcacccag ttcatgaccc agaactacca ggactcacca 700

accctccagg ctcccagagg aagggccagc gagcccaagc acaaaaccag 750

gcagagatag ctgcctgcta gatagccggc tttgccatcc gggcatgtgg 800

ccacactgct caccaccgac gatgtgggta tggaacccccc tctggataca 850

gaaccccttc ttttccaaat taaaaaaaaa aatcatcaaa 890
```

<210> 61
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52

<211> 223
<212> PRT
<213> Homo Sapien

<400> 61
Met Gly Trp Thr Met Arg Leu Val Thr Ala Ala Leu Leu Leu Gly
1               5                   10                  15

Leu Met Met Val Val Thr Gly Asp Glu Asp Glu Asn Ser Pro Cys
                20                  25                  30

Ala His Glu Ala Leu Leu Asp Glu Asp Thr Leu Phe Cys Gln Gly
                35                  40                  45

Leu Glu Val Phe Tyr Pro Glu Leu Gly Asn Ile Gly Cys Lys Val
                50                  55                  60

Val Pro Asp Cys Asn Asn Tyr Arg Gln Lys Ile Thr Ser Trp Met
                65                  70                  75

Glu Pro Ile Val Lys Phe Pro Gly Ala Val Asp Gly Ala Thr Tyr
                80                  85                  90

Ile Leu Val Met Val Asp Pro Asp Ala Pro Ser Arg Ala Glu Pro
                95                  100                 105

Arg Gln Arg Phe Trp Arg His Trp Leu Val Thr Asp Ile Lys Gly
                110                 115                 120

Ala Asp Leu Lys Lys Gly Lys Ile Gln Gly Gln Glu Leu Ser Ala
                125                 130                 135

Tyr Gln Ala Pro Ser Pro Pro Ala His Ser Gly Phe His Arg Tyr
                140                 145                 150

Gln Phe Phe Val Tyr Leu Gln Glu Gly Lys Val Ile Ser Leu Leu
                155                 160                 165

Pro Lys Glu Asn Lys Thr Arg Gly Ser Trp Lys Met Asp Arg Phe
                170                 175                 180

Leu Asn Arg Phe His Leu Gly Glu Pro Glu Ala Ser Thr Gln Phe
                185                 190                 195

Met Thr Gln Asn Tyr Gln Asp Ser Pro Thr Leu Gln Ala Pro Arg
                200                 205                 210

Gly Arg Ala Ser Glu Pro Lys His Lys Thr Arg Gln Arg
                215                 220

<210> 62
<211> 1321
<212> DNA
<213> Homo Sapien

<400> 62
gtcgacccac gcgtccgaag ctgctggagc cacgattcag tcccctggac 50

53

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tgtagataaa gaccctttct tgccaggtgc tgagacaacc acactatgag 100

aggcactcca ggagacgctg atggtggagg aagggccgtc tatcaatcaa 150

tcactgttgc tgttatcaca tgcaagtatc cagaggctct tgagcaaggc 200

agaggggatc ccatttattt gggaatccag aatccagaaa tgtgtttgta 250

ttgtgagaag gttggagaac agcccacatt gcagctaaaa gagcagaaga 300

tcatggatct gtatggccaa cccgagcccg tgaaacccct ccttttctac 350

cgtgccaaga ctggtaggac ctccaccctt gagtctgtgg ccttcccgga 400

ctggttcatt gcctcctcca agagagacca gcccatcatt ctgacttcag 450

aacttgggaa gtcatacaac actgcctttg aattaaatat aaatgactga 500

actcagccta gaggtggcag cttggtcttt gtcttaaagt ttctggttcc 550

caatgtgttt tcgtctacat tttcttagtg tcattttcac gctggtgctg 600

agacaggagc aaggctgctg ttatcatctc attttataat gaagaagaag 650

caattacttc atagcaactg aagaacagga tgtggcctca gaagcaggag 700

agctgggtgg tataaggctg tcctctcaag ctggtgctgt gtaggccaca 750

aggcatctgc atgagtgact ttaagactca aagaccaaac actgagcttt 800

cttctagggg tgggtatgaa gatgcttcag agctcatgcg cgttacccac 850

gatggcatga ctagcacaga gctgatctct gtttctgttt tgctttattc 900

cctcttggga tgatatcatc cagtctttat atgttgccaa tatacctcat 950

tgtgtgtaat agaaccttct tagcattaag accttgtaaa caaaaataat 1000

tcttggggtg ggtatgaaga tgcttcagag ctcatgcgcg ttacccacga 1050

tggcatgact agcacagagc tgatctctgt ttctgttttg ctttattccc 1100

tcttgggatg atatcatcca gtctttatat gttgccaata tacctcattg 1150

tgtgtaatag aaccttctta gcattaagac cttgtaaaca aaataattc 1200

ttgtgttaag ttaaatcatt tttgtcctaa ttgtaatgtg taatcttaaa 1250

gttaaataaa ctttgtgtat ttatataata ataaagctaa aactgatata 1300

aaataaagaa agagtaaact g 1321

<210> 63
<211> 134
<212> PRT
<213> Homo Sapien

<400> 63
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54

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Met Arg Gly Thr Pro Gly Asp Ala Asp Gly Gly Gly Arg Ala Val
  1               5                  10                  15

Tyr Gln Ser Ile Thr Val Ala Val Ile Thr Cys Lys Tyr Pro Glu
               20                  25                  30

Ala Leu Glu Gln Gly Arg Gly Asp Pro Ile Tyr Leu Gly Ile Gln
               35                  40                  45

Asn Pro Glu Met Cys Leu Tyr Cys Glu Lys Val Gly Glu Gln Pro
               50                  55                  60

Thr Leu Gln Leu Lys Glu Gln Lys Ile Met Asp Leu Tyr Gly Gln
               65                  70                  75

Pro Glu Pro Val Lys Pro Phe Leu Phe Tyr Arg Ala Lys Thr Gly
               80                  85                  90

Arg Thr Ser Thr Leu Glu Ser Val Ala Phe Pro Asp Trp Phe Ile
               95                 100                 105

Ala Ser Ser Lys Arg Asp Gln Pro Ile Ile Leu Thr Ser Glu Leu
              110                 115                 120

Gly Lys Ser Tyr Asn Thr Ala Phe Glu Leu Asn Ile Asn Asp
              125                 130

<210> 64
<211> 999
<212> DNA
<213> Homo Sapien

<400> 64
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 gtgctgctgc tgctcctggc gggagccccc gccgcgcggc ccactccccc 100

 gacctgctac tcccgcatgc gggccctgag ccaggagatc acccgcgact 150

 tcaacctcct gcaggtctcg gagccctcgg agccatgtgt gagatacctg 200

 cccaggctgt acctggacat acacaattac tgtgtgctgg acaagctgcg 250

 ggactttgtg gcctcgcccc cgtgttggaa agtggcccag gtagattcct 300

 tgaaggacaa agcacggaag ctgtacacca tcatgaactc gttctgcagg 350

 agagatttgg tattcctgtt ggatgactgc aatgccttgg aatacccaat 400

 cccagtgact acggtcctgc agatcgtca gcgctaaggg aactgagacc 450

 agagaaagaa cccaagagaa ctaaagttat gtcagctacc cagacttaat 500

 gggccagagc catgaccctc acaggtcttg tgttagttgt atctgaaact 550

 gttatgtatc tctctacctt ctggaaaaca gggctggtat cctacccag 600

 gaacctcctt tgagcataga gttagcaacc atgcttctca ttcccttgac 650
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55

tcatgtcttg ccaggatggt tagatacaca gcatgttgat ttggtcacta 700

aaaagaagaa aaggactaac aagcttcact tttatgaaca actattttga 750

gaacatgcac aatagtatgt ttttattact ggtttaatgg agtaatggta 800

cttttattct ttcttgatag aaacctgctt acatttaacc aagcttctat 850

tatgcctttt tctaacacag actttcttca ctgtctttca tttaaaaaga 900

aattaatgct cttaagatat atattttacg tagtgctgac aggacccact 950

ctttcattga aaggtgatga aaatcaaata aagaatctct tcacatgga 999

<210> 65
<211> 136
<212> PRT
<213> Homo Sapien

<400> 65
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Met Arg Thr Pro Gly Pro Leu Pro Val Leu Leu Leu Leu Ala
  1               5                  10                  15

Gly Ala Pro Ala Ala Arg Pro Thr Pro Pro Thr Cys Tyr Ser Arg
                20                  25                  30

Met Arg Ala Leu Ser Gln Glu Ile Thr Arg Asp Phe Asn Leu Leu
                35                  40                  45

Gln Val Ser Glu Pro Ser Glu Pro Cys Val Arg Tyr Leu Pro Arg
                50                  55                  60

Leu Tyr Leu Asp Ile His Asn Tyr Cys Val Leu Asp Lys Leu Arg
                65                  70                  75

Asp Phe Val Ala Ser Pro Pro Cys Trp Lys Val Ala Gln Val Asp
                80                  85                  90

Ser Leu Lys Asp Lys Ala Arg Lys Leu Tyr Thr Ile Met Asn Ser
                95                  100                 105

Phe Cys Arg Arg Asp Leu Val Phe Leu Leu Asp Asp Cys Asn Ala
                110                 115                 120

Leu Glu Tyr Pro Ile Pro Val Thr Thr Val Leu Pro Asp Arg Gln
                125                 130                 135

Arg
```

<210> 66
<211> 1893
<212> DNA
<213> Homo Sapien

<400> 66
gtctccgcgt cacaggaact tcagcaccca cagggcggac agcgctcccc 50

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tctacctgga gacttgactc ccgcgcgccc caaccctgct tatcccttga 100

ccgtcgagtg tcagagatcc tgcagccgcc cagtcccggc ccctctcccg 150

ccccacaccc accctcctgg ctcttcctgt ttttactcct ccttttcatt 200

cataacaaaa gctacagctc caggagccca gcgccgggct gtgacccaag 250

ccgagcgtgg aagaatgggg ttcctcggga ccggcacttg gattctggtg 300

ttagtgctcc cgattcaagc tttccccaaa cctggaggaa gccaagacaa 350

atctctacat aatagagaat taagtgcaga aagacctttg aatgaacaga 400

ttgctgaagc agaagaagac aagattaaaa aaacatatcc tccagaaaac 450

aagccaggtc agagcaacta ttcttttgtt gataacttga acctgctaaa 500

ggcaataaca gaaaaggaaa aaattgagaa agaaagacaa tctataagaa 550

gctcccccact tgataataag ttgaatgtgg aagatgttga ttcaaccaag 600

aatcgaaaac tgatcgatga ttatgactct actaagagtg gattggatca 650

taaatttcaa gatgatccag atggtcttca tcaactagac gggactcctt 700

taaccgctga agacattgtc cataaaatcg ctgccaggat ttatgaagaa 750

aatgacagag ccgtgtttga caagattgtt tctaaactac ttaatctcgg 800

ccttatcaca gaaagccaag cacatacact ggaagatgaa gtagcagagg 850

ttttacaaaa attaatctca aaggaagcca caattatga ggaggatccc 900

aataagccca caagctggac tgagaatcag gctggaaaaa taccagagaa 950

agtgactcca atggcagcaa ttcaagatgg tcttgctaag ggagaaaacg 1000

atgaaacagt atctaacaca ttaaccttga caaatggctt ggaaaggaga 1050

actaaaacct acagtgaaga caactttgag gaactccaat atttcccaaa 1100

tttctatgcg ctactgaaaa gtattgattc agaaaaagaa gcaaaagaga 1150

aagaaacact gattactatc atgaaaacac tgattgactt tgtgaagatg 1200

atggtgaaat atggaacaat atctccagaa gaaggtgttt cctaccttga 1250

aaacttggat gaaatgattg ctcttcagac caaaaacaag ctagaaaaaa 1300

atgctactga caatataagc aagctttttcc cagcaccatc agagaagagt 1350

catgaagaaa cagacagtac caaggaagaa gcagctaaga tggaaaagga 1400

atatggaagc ttgaaggatt ccacaaaaga tgataactcc aacccaggag 1450

gaaagacaga tgaacccaaa ggaaaaacag aagcctattt ggaagccatc 1500
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57

agaaaaaata ttgaatggtt gaagaaacat gacaaaaagg gaaataaaga 1550

agattatgac ctttcaaaga tgagagactt catcaataaa caagctgatg 1600

cttatgtgga gaaaggcatc cttgacaagg aagaagccga ggccatcaag 1650

cgcatttata gcagcctgta aaaatggcaa aagatccagg agtctttcaa 1700

ctgtttcaga aaacataata tagcttaaaa cacttctaat tctgtgatta 1750

aaattttttg acccaagggt tattagaaag tgctgaattt acagtagtta 1800

acctttaca agtggttaaa acatagcttt cttcccgtaa aaactatctg 1850

aaagtaaagt tgtatgtaag ctgaaaaaaa aaaaaaaaaa aaa 1893

<210> 67
<211> 468
<212> PRT
<213> Homo Sapien

<400> 67
Met Gly Phe Leu Gly Thr Gly Thr Trp Ile Leu Val Leu Val Leu
  1   5   10   15

Pro Ile Gln Ala Phe Pro Lys Pro Gly Gly Ser Gln Asp Lys Ser
                 20   25   30

Leu His Asn Arg Glu Leu Ser Ala Glu Arg Pro Leu Asn Glu Gln
                 35   40   45

Ile Ala Glu Ala Glu Glu Asp Lys Ile Lys Lys Thr Tyr Pro Pro
                 50   55   60

Glu Asn Lys Pro Gly Gln Ser Asn Tyr Ser Phe Val Asp Asn Leu
                 65   70   75

Asn Leu Leu Lys Ala Ile Thr Glu Lys Glu Lys Ile Glu Lys Glu
                 80   85   90

Arg Gln Ser Ile Arg Ser Ser Pro Leu Asp Asn Lys Leu Asn Val
                 95   100   105

Glu Asp Val Asp Ser Thr Lys Asn Arg Lys Leu Ile Asp Asp Tyr
                110   115   120

Asp Ser Thr Lys Ser Gly Leu Asp His Lys Phe Gln Asp Asp Pro
                125   130   135

Asp Gly Leu His Gln Leu Asp Gly Thr Pro Leu Thr Ala Glu Asp
                140   145   150

Ile Val His Lys Ile Ala Ala Arg Ile Tyr Glu Glu Asn Asp Arg
                155   160   165

Ala Val Phe Asp Lys Ile Val Ser Lys Leu Leu Asn Leu Gly Leu
                170   175   180

58

Ile Thr Glu Ser Gln Ala His Thr Leu Glu Asp Glu Val Ala Glu
                185   190   195

Val Leu Gln Lys Leu Ile Ser Lys Glu Ala Asn Asn Tyr Glu Glu
                200   205   210

Asp Pro Asn Lys Pro Thr Ser Trp Thr Glu Asn Gln Ala Gly Lys
                215   220   225

Ile Pro Glu Lys Val Thr Pro Met Ala Ala Ile Gln Asp Gly Leu
                230   235   240

Ala Lys Gly Glu Asn Asp Glu Thr Val Ser Asn Thr Leu Thr Leu
                245   250   255

Thr Asn Gly Leu Glu Arg Arg Thr Lys Thr Tyr Ser Glu Asp Asn
                260   265   270

Phe Glu Glu Leu Gln Tyr Phe Pro Asn Phe Tyr Ala Leu Leu Lys
                275   280   285

Ser Ile Asp Ser Glu Lys Glu Ala Lys Glu Lys Glu Thr Leu Ile
                290   295   300

Thr Ile Met Lys Thr Leu Ile Asp Phe Val Lys Met Met Val Lys
                305   310   315

Tyr Gly Thr Ile Ser Pro Glu Glu Gly Val Ser Tyr Leu Glu Asn
                320   325   330

Leu Asp Glu Met Ile Ala Leu Gln Thr Lys Asn Lys Leu Glu Lys
                335   340   345

Asn Ala Thr Asp Asn Ile Ser Lys Leu Phe Pro Ala Pro Ser Glu
                350   355   360

Lys Ser His Glu Glu Thr Asp Ser Thr Lys Glu Glu Ala Ala Lys
                365   370   375

Met Glu Lys Glu Tyr Gly Ser Leu Lys Asp Ser Thr Lys Asp Asp
                380   385   390

Asn Ser Asn Pro Gly Gly Lys Thr Asp Glu Pro Lys Gly Lys Thr
                395   400   405

Glu Ala Tyr Leu Glu Ala Ile Arg Lys Asn Ile Glu Trp Leu Lys
                410   415   420

Lys His Asp Lys Lys Gly Asn Lys Glu Asp Tyr Asp Leu Ser Lys
                425   430   435

Met Arg Asp Phe Ile Asn Lys Gln Ala Asp Ala Tyr Val Glu Lys
                440   445   450

Gly Ile Leu Asp Lys Glu Glu Ala Glu Ala Ile Lys Arg Ile Tyr
                455   460   465

Ser Ser Leu

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<210> 68
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 68
 cgtcacagga acttcagcac cc 22

<210> 69
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 69
 gtcttggctt cctccaggtt tgg 23

<210> 70
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 70
 ggacagcgct cccctctacc tggagacttg actcccgc 38

<210> 71
<211> 2379
<212> DNA
<213> Homo Sapien

<400> 71
 gttgctccgg cggcgctcgg ggagggagcc agcagcctag ggcctaggcc 50

 cgggccacca tggcgctgcc tccaggccca gccgccctcc ggcacacact 100

 gctgctcctg ccagcccttc tgagctcagg ttggggggag ttggagccac 150

 aaatagatgg tcagacctgg ctgagcggg cacttcggga gaatgaacgc 200

 cacgccttca cctgccgggt ggcagggggg cctggcaccc ccagattggc 250

 ctggtatctg gatggacagc tgcaggaggc cagcacctca agactgctga 300

 gcgtgggagg ggaggccttc tctggaggca ccagcacctt cactgtcact 350

 gcccatcggg cccagcatga gctcaactgc tctctgcagg accccagaag 400

 tggccgatca gccaacgcct ctgtcatcct taatgtgcaa ttcaagccag 450
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agattgccca agtcggcgcc aagtaccagg aagctcaggg cccaggcctc 500

ctggttgtcc tgtttgccct ggtgcgtgcc aacccgccgg ccaatgtcac 550

ctggatcgac caggatgggc cagtgactgt caacacctct gacttcctgg 600

tgctggatgc gcagaactac ccctggctca ccaaccacac ggtgcagctg 650

cagctccgca gcctggcaca caacctctcg gtggtggcca ccaatgacgt 700

gggtgtcacc agtgcgtcgc ttccagcccc aggcccctcc cggcacccat 750

ctctgatatc aagtgactcc aacaacctaa aactcaacaa cgtgcgcctg 800

ccacgggaga acatgtccct cccgtccaac cttcagctca atgacctcac 850

tccagattcc agagcagtga aaccagcaga ccggcagatg gctcagaaca 900

acagccggcc agagcttctg gacccggagc ccggcggcct cctcaccagc 950

caaggtttca tccgcctccc agtgctgggc tatatctatc gagtgtccag 1000

cgtgagcagt gatgagatct ggctctgagc cgagggcgag acaggagtat 1050

tctcttggcc tctggacacc ctcccattcc tccaaggcat cctctaccta 1100

gctaggtcac caacgtgaag aagttatgcc actgccactt ttgcttgccc 1150

tcctggctgg ggtgccctcc atgtcatgca cgtgatgcat ttcactgggc 1200

tgtaacccgc aggggcacag gtatctttgg caaggctacc agttggacgt 1250

aagcccctca tgctgactca gggtgggccc tgcatgtgat gactgggccc 1300

ttccagaggg agctctttgg ccaggggtgt tcagatgtca tccagcatcc 1350

aagtgtggca tggcctgctg tataccccac cccagtactc cacagcacct 1400

tgtacagtag gcatgggggc gtgcctgtgt gggggacagg gagggccctg 1450

catggatttt cctccttcct atgctatgta gccttgttcc ctcaggtaaa 1500

atttaggacc ctgctagctg tgcagaaccc aattgccctt tgcacagaaa 1550

ccaacccctg acccagcggt accggccaag cacaaacgtc cttttgctg 1600

cacacgtctc tgcccttcac ttcttctctt ctgtccccac ctcctcttgg 1650

gaattctagg ttacacgttg gaccttctct actacttcac tgggcactag 1700

acttttctat tggcctgtgc catcgcccag tattagcaca agttagggag 1750

gaagaggcag gcgatgagtc tagtagcacc caggacggct tgtagctatg 1800

catcattttc ctacggcgtt agcactttaa gcacatcccc tagggaggg 1850

ggtgagtgag gggcccagag ccctctttgt ggcttcccca cgtttggcct 1900
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61

tctgggattc actgtgagtg tcctgagctc tcggggttga tggtttttct 1950

ctcagcatgt ctcctccacc acgggacccc agccctgacc aacccatggt 2000

tgcctcatca gcaggaaggt gcccttcctg gaggatggtc gccacaggca 2050

cataattcaa cagtgtggaa gctttagggg aacatggaga agaaggaga 2100

ccacataccc caaagtgacc taagaacact ttaaaaagca acatgtaaat 2150

gattggaaat taatatagta cagaatatat ttttcccttg ttgagatctt 2200

cttttgtaat gtttttcatg ttactgccta gggcggtgct gagcacacag 2250

caagtttaat aaacttgact gaattcattt aaaaaaaaaa aaaaaaaaaa 2300

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2350

aaaaaaaaaa aaaaaaaaaa aaaaaaaaa 2379

<210> 72
<211> 322
<212> PRT
<213> Homo Sapien

<400> 72
Met Ala Leu Pro Pro Gly Pro Ala Ala Leu Arg His Thr Leu Leu
 1   5   10   15

Leu Leu Pro Ala Leu Leu Ser Ser Gly Trp Gly Glu Leu Glu Pro
                20   25   30

Gln Ile Asp Gly Gln Thr Trp Ala Glu Arg Ala Leu Arg Glu Asn
                35   40   45

Glu Arg His Ala Phe Thr Cys Arg Val Ala Gly Gly Pro Gly Thr
                50   55   60

Pro Arg Leu Ala Trp Tyr Leu Asp Gly Gln Leu Gln Glu Ala Ser
                65   70   75

Thr Ser Arg Leu Leu Ser Val Gly Gly Glu Ala Phe Ser Gly Gly
                80   85   90

Thr Ser Thr Phe Thr Val Thr Ala His Arg Ala Gln His Glu Leu
                95   100   105

Asn Cys Ser Leu Gln Asp Pro Arg Ser Gly Arg Ser Ala Asn Ala
                110   115   120

Ser Val Ile Leu Asn Val Gln Phe Lys Pro Glu Ile Ala Gln Val
                125   130   135

Gly Ala Lys Tyr Gln Glu Ala Gln Gly Pro Gly Leu Leu Val Val
                140   145   150

Leu Phe Ala Leu Val Arg Ala Asn Pro Pro Ala Asn Val Thr Trp
                155   160   165

62

```
Ile Asp Gln Asp Gly Pro Val Thr Val Asn Thr Ser Asp Phe Leu
                170                 175                 180

Val Leu Asp Ala Gln Asn Tyr Pro Trp Leu Thr Asn His Thr Val
                185                 190                 195

Gln Leu Gln Leu Arg Ser Leu Ala His Asn Leu Ser Val Val Ala
                200                 205                 210

Thr Asn Asp Val Gly Val Thr Ser Ala Ser Leu Pro Ala Pro Gly
                215                 220                 225

Pro Ser Arg His Pro Ser Leu Ile Ser Ser Asp Ser Asn Asn Leu
                230                 235                 240

Lys Leu Asn Asn Val Arg Leu Pro Arg Glu Asn Met Ser Leu Pro
                245                 250                 255

Ser Asn Leu Gln Leu Asn Asp Leu Thr Pro Asp Ser Arg Ala Val
                260                 265                 270

Lys Pro Ala Asp Arg Gln Met Ala Gln Asn Asn Ser Arg Pro Glu
                275                 280                 285

Leu Leu Asp Pro Glu Pro Gly Gly Leu Leu Thr Ser Gln Gly Phe
                290                 295                 300

Ile Arg Leu Pro Val Leu Gly Tyr Ile Tyr Arg Val Ser Ser Val
                305                 310                 315

Ser Ser Asp Glu Ile Trp Leu
                320
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<210> 73
<211> 843
<212> DNA
<213> Homo Sapien

<400> 73
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cggggacgga agcggcccct gggcccgagg ggctggagcc gggccggggc 50

gatgtggagc gcgggccgcg gcggggctgc ctggccggtg ctgttggggc 100

tgctgctggc gctgttagtg ccgggcggtg gtgccgccaa gaccggtgcg 150

gagctcgtga cctgcgggtc ggtgctgaag ctgctcaata cgcaccaccg 200

cgtgcggctg cactcgcacg acatcaaata cggatccggc agcggccagc 250

aatcggtgac cggcgtagag gcgtcggacg acgccaatag ctactggcgg 300

atccgcggcg gctcggaggg cgggtgcccg cgcgggtccc cggtgcgctg 350

cgggcaggcg gtgaggctca cgcatgtgct tacgggcaag aacctgcaca 400

cgcaccactt cccgtcgccg ctgtccaaca accaggaggt gagtgccttt 450

ggggaagacg gcgagggcga cgacctggac ctatggacag tgcgctgctc 500
```

63

```
tggacagcac tgggagcgtg aggctgctgt gcgcttccag catgtgggca 550

cctctgtgtt cctgtcagtc acgggtgagc agtatggaag ccccatccgt 600

gggcagcatg aggtccacgg catgcccagt gccaacacgc acaatacgtg 650

gaaggccatg gaaggcatct tcatcaagcc tagtgtggag ccctctgcag 700

gtcacgatga actctgagtg tgtggatgga tgggtggatg gagggtggca 750

ggtggggcgt ctgcagggcc actcttggca gagactttgg gtttgtaggg 800

gtcctcaagt gcctttgtga ttaaagaatg ttggtctatg aaa 843
```

<210> 74
<211> 221
<212> PRT
<213> Homo Sapien

<400> 74

```
Met Trp Ser Ala Gly Arg Gly Gly Ala Ala Trp Pro Val Leu Leu
 1               5                  10                  15

Gly Leu Leu Leu Ala Leu Leu Val Pro Gly Gly Gly Ala Ala Lys
                20                  25                  30

Thr Gly Ala Glu Leu Val Thr Cys Gly Ser Val Leu Lys Leu Leu
                35                  40                  45

Asn Thr His His Arg Val Arg Leu His Ser His Asp Ile Lys Tyr
                50                  55                  60

Gly Ser Gly Ser Gly Gln Gln Ser Val Thr Gly Val Glu Ala Ser
                65                  70                  75

Asp Asp Ala Asn Ser Tyr Trp Arg Ile Arg Gly Gly Ser Glu Gly
                80                  85                  90

Gly Cys Pro Arg Gly Ser Pro Val Arg Cys Gly Gln Ala Val Arg
                95                  100                 105

Leu Thr His Val Leu Thr Gly Lys Asn Leu His Thr His His Phe
                110                 115                 120

Pro Ser Pro Leu Ser Asn Asn Gln Glu Val Ser Ala Phe Gly Glu
                125                 130                 135

Asp Gly Glu Gly Asp Asp Leu Asp Leu Trp Thr Val Arg Cys Ser
                140                 145                 150

Gly Gln His Trp Glu Arg Glu Ala Ala Val Arg Phe Gln His Val
                155                 160                 165

Gly Thr Ser Val Phe Leu Ser Val Thr Gly Glu Gln Tyr Gly Ser
                170                 175                 180

Pro Ile Arg Gly Gln His Glu Val His Gly Met Pro Ser Ala Asn
                185                 190                 195
```

64

Thr His Asn Thr Trp Lys Ala Met Glu Gly Ile Phe Ile Lys Pro
              200   205   210

Ser Val Glu Pro Ser Ala Gly His Asp Glu Leu
              215   220

<210> 75
<211> 1049
<212> DNA
<213> Homo Sapien

<400> 75
gttgctatgt tgcccaggct ggtcttgaag tgccttgacc tcctaaagtg 50

ttggaaccac agacgtgagc cactccaccc agcctaaaac ttcatcttct 100

ttggatgaga tgaacacttt taacaagaga acaggactct atataaatcg 150

ctgtgggctc accacctcta aggaggagca ctgactgaag acagaaaaat 200

tgatgaactg aagaagacat ggtccattat gccttacaaa cttacacagt 250

gctttgggaa ttccaaagta ctcagtggag agaggtgttt caggagccgt 300

agagccagat cgtcatcatg tctgcattgt ggctgctgct gggcctcctt 350

gccctgatgg acttgtctga aagcagcaac tggggatgct atggaaacat 400

ccaaagcctg gacacccctg agcatcttg tgggattgga agacgtcacg 450

gcctgaacta ctgtggagtt cgtgcttctg aaaggctggc tgaaatagac 500

atgccatacc tcctgaaata tcaacccatg atgcaaacca ttggccaaaa 550

gtactgcatg gatcctgccg tgatcgctgg tgtcttgtcc aggaagtctc 600

ccggtgacaa aattctggtc aacatgggcg ataggactag catggtgcag 650

gaccctggct ctcaagctcc cacatcctgg attagtgagt ctcaggtttc 700

ccagacaact gaagttctga ctactagaat caaagaaatc cagaggaggt 750

ttccaacctg gacccctgac cagtacctga gaggtggact ctgtgcctac 800

agtgggggtg ctggctatgt ccgaagcagc caggacctga gctgtgactt 850

ctgcaatgat gtccttgcac gagccaagta cctcaagaga catggcttct 900

aacatctcag atgaaaccca agaccatgat cacatatgca gcctcaaatg 950

ttacacagat aaaactagcc aagggcacct gtaactggga atctgagttt 1000

gacctaaaag tcattaaaat aacatgaatc ccattaaaaa aaaaaaaaa 1049

<210> 76
<211> 194
<212> PRT
<213> Homo Sapien

<400> 76
```
Met Ser Ala Leu Trp Leu Leu Leu Gly Leu Leu Ala Leu Met Asp
  1               5                  10                  15

Leu Ser Glu Ser Ser Asn Trp Gly Cys Tyr Gly Asn Ile Gln Ser
               20                  25                  30

Leu Asp Thr Pro Gly Ala Ser Cys Gly Ile Gly Arg Arg His Gly
               35                  40                  45

Leu Asn Tyr Cys Gly Val Arg Ala Ser Glu Arg Leu Ala Glu Ile
               50                  55                  60

Asp Met Pro Tyr Leu Leu Lys Tyr Gln Pro Met Met Gln Thr Ile
               65                  70                  75

Gly Gln Lys Tyr Cys Met Asp Pro Ala Val Ile Ala Gly Val Leu
               80                  85                  90

Ser Arg Lys Ser Pro Gly Asp Lys Ile Leu Val Asn Met Gly Asp
               95                 100                 105

Arg Thr Ser Met Val Gln Asp Pro Gly Ser Gln Ala Pro Thr Ser
              110                 115                 120

Trp Ile Ser Glu Ser Gln Val Ser Gln Thr Thr Glu Val Leu Thr
              125                 130                 135

Thr Arg Ile Lys Glu Ile Gln Arg Arg Phe Pro Thr Trp Thr Pro
              140                 145                 150

Asp Gln Tyr Leu Arg Gly Gly Leu Cys Ala Tyr Ser Gly Gly Ala
              155                 160                 165

Gly Tyr Val Arg Ser Ser Gln Asp Leu Ser Cys Asp Phe Cys Asn
              170                 175                 180

Asp Val Leu Ala Arg Ala Lys Tyr Leu Lys Arg His Gly Phe
              185                 190
```

<210> 77
<211> 899
<212> DNA
<213> Homo Sapien

<400> 77
```
ttgaaaatct actctatcag ctgctgtggt tgccaccatt ctcaggaccc 50

tcgccatgaa agcccttatg ctgctcaccc tgtctgttct gctctgctgg 100

gtctcagctg acattcgctg tcactcctgc tacaaggtcc ctgtgctggg 150

ctgtgtggac cggcagtcct gccgcctgga gccaggacag caatgcctga 200

caacacatgc ataccttggt aagatgtggg ttttctccaa tctgcgctgt 250

ggcacaccag aagagccctg tcaggaggcc ttcaaccaaa ccaaccgcaa 300
```

66

```
gctgggtctg acatataaca ccacctgctg caacaaggac aactgcaaca 350

gcgcaggacc ccggcccact ccagccctgg gccttgtctt ccttacctcc 400

ttggctggcc ttggcctctg gctgctgcac tgagactcat tccattggct 450

gcccctcctc ccacctgcct tggcctgagc ctctctccct gtgtctctgt 500

atcccctggc tttacagaat cgtctctccc tagctcccat ttctttaatt 550

aaacactgtt ccgagtggtc tcctcatcca tccttcccac ctcacaccct 600

tcactctcct ttttctgggt cccttcccac ttccttccag gacctccatt 650

ggctcctaga agggctcccc actttgcttc ctatactctg ctgtccccta 700

cttgaggagg gattgggatc tgggcctgaa atggggcttc tgtgttgtcc 750

ccagtgaagg ctcccacaag gacctgatga cctcactgta cagagctgac 800

tccccaaacc caggctccca tatgtacccc atcccccata ctcacctctt 850

tccattttga gtaataaatg tctgagtctg gaaaaaaaaa aaaaaaaaa 899
```

<210> 78
<211> 125
<212> PRT
<213> Homo Sapien

<400> 78
```
Met Lys Ala Leu Met Leu Leu Thr Leu Ser Val Leu Leu Cys Trp
 1               5                  10                  15

Val Ser Ala Asp Ile Arg Cys His Ser Cys Tyr Lys Val Pro Val
                20                  25                  30

Leu Gly Cys Val Asp Arg Gln Ser Cys Arg Leu Glu Pro Gly Gln
                35                  40                  45

Gln Cys Leu Thr Thr His Ala Tyr Leu Gly Lys Met Trp Val Phe
                50                  55                  60

Ser Asn Leu Arg Cys Gly Thr Pro Glu Glu Pro Cys Gln Glu Ala
                65                  70                  75

Phe Asn Gln Thr Asn Arg Lys Leu Gly Leu Thr Tyr Asn Thr Thr
                80                  85                  90

Cys Cys Asn Lys Asp Asn Cys Asn Ser Ala Gly Pro Arg Pro Thr
                95                  100                 105

Pro Ala Leu Gly Leu Val Phe Leu Thr Ser Leu Ala Gly Leu Gly
                110                 115                 120

Leu Trp Leu Leu His
                125
```

<210> 79
```

67

<400> 79

```
acgggccgca gcggcagtga cgtagggttg gcgcacggat ccgttgcggc 50

tgcagctctg cagtcgggcc gttccttcgc cgccgccagg ggtagcggtg 100

tagctgcgca gcgtcgcgcg cgctaccgca cccaggttcg gcccgtaggc 150

gtctggcagc ccggcgccat cttcatcgag cgccatggcc gcagcctgcg 200

ggccgggagc ggccgggtac tgcttgctcc tcggcttgca tttgtttctg 250

ctgaccgcgg gccctgccct gggctggaac gaccctgaca gaatgttgct 300

gcgggatgta aaagctctta ccctccacta tgaccgctat accacctccc 350

gcaggctgga tcccatccca cagttgaaat gtgttggagg cacagctggt 400

tgtgattctt ataccccaaa agtcatacag tgtcagaaca aaggctggga 450

tgggtatgat gtacagtggg aatgtaagac ggacttagat attgcataca 500

aatttggaaa aactgtggtg agctgtgaag gctatgagtc ctctgaagac 550

cagtatgtac taagaggttc ttgtggcttg gagtataatt tagattatac 600

agaacttggc ctgcagaaac tgaaggagtc tggaaagcag cacggctttg 650

cctctttctc tgattattat tataagtggt cctcggcgga ttcctgtaac 700

atgagtggat tgattaccat cgtggtactc cttgggatcg cctttgtagt 750

ctataagctg ttcctgagtg acgggcagta ttctcctcca ccgtactctg 800

agtatcctcc attttcccac cgttaccaga gattcaccaa ctcagcagga 850

cctcctcccc caggctttaa gtctgagttc acaggaccac agaatactgg 900

ccatggtgca acttctggtt ttggcagtgc ttttacagga caacaaggat 950

atgaaaattc aggaccaggg ttctggacag gcttgggaac tggtggaata 1000

ctaggatatt tgtttggcag caatagagcg gcaacaccct tctcagactc 1050

gtggtactac ccgtcctatc ctccctccta ccctggcacg tggaataggg 1100

cttactcacc ccttcatgga ggctcgggca gctattcggt atgttcaaac 1150

tcagacacga aaaccagaac tgcatcagga tatggtggta ccaggagacg 1200

ataaagtaga aagttggagt caaacactgg atgcagaaat tttggatttt 1250

tcatcacttt ctctttagaa aaaaagtact acctgttaac aattgggaaa 1300

aggggatatt caaaagttct gtggtgttat gtccagtgta gctttttgta 1350
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68

ttctattatt tgaggctaaa agttgatgtg tgacaaaata cttatgtgtt 1400

gtatgtcagt gtaacatgca gatgtatatt gcagtttttg aaagtgatca 1450

ttactgtgga atgctaaaaa tacattaatt tctaaaacct gtgatgccct 1500

aagaagcatt aagaatgaag gtgttgtact aatagaaact aagtacagaa 1550

aatttcagtt ttaggtggtt gtagctgatg agttattacc tcatagagac 1600

tataatattc tatttggtat tatattattt gatgtttgct gttcttcaaa 1650

catttaaatc aagctttgga ctaattatgc taatttgtga gttctgatca 1700

cttttgagct ctgaagcttt gaatcattca gtggtggaga tggccttctg 1750

gtaactgaat attaccttct gtaggaaaag gtggaaaata agcatctaga 1800

aggttgttgt gaatgactct gtgctggcaa aaatgcttga aacctctata 1850

tttctttcgt tcataagagg taaaggtcaa attttttcaac aaaagtcttt 1900

taataacaaa agcatgcagt tctctgtgaa atctcaaata ttgttgtaat 1950

agtctgtttc aatcttaaaa agaatca 1977

<210> 80
<211> 339
<212> PRT
<213> Homo Sapien

<400> 80
Met Ala Ala Ala Cys Gly Pro Gly Ala Ala Gly Tyr Cys Leu Leu
  1   5   10   15

Leu Gly Leu His Leu Phe Leu Leu Thr Ala Gly Pro Ala Leu Gly
                 20   25   30

Trp Asn Asp Pro Asp Arg Met Leu Leu Arg Asp Val Lys Ala Leu
                 35   40   45

Thr Leu His Tyr Asp Arg Tyr Thr Thr Ser Arg Arg Leu Asp Pro
                 50   55   60

Ile Pro Gln Leu Lys Cys Val Gly Gly Thr Ala Gly Cys Asp Ser
                 65   70   75

Tyr Thr Pro Lys Val Ile Gln Cys Gln Asn Lys Gly Trp Asp Gly
                 80   85   90

Tyr Asp Val Gln Trp Glu Cys Lys Thr Asp Leu Asp Ile Ala Tyr
                 95   100   105

Lys Phe Gly Lys Thr Val Val Ser Cys Glu Gly Tyr Glu Ser Ser
                 110   115   120

Glu Asp Gln Tyr Val Leu Arg Gly Ser Cys Gly Leu Glu Tyr Asn
                 125   130   135

69

```
Leu Asp Tyr Thr Glu Leu Gly Leu Gln Lys Leu Lys Glu Ser Gly
             140              145              150

Lys Gln His Gly Phe Ala Ser Phe Ser Asp Tyr Tyr Tyr Lys Trp
             155              160              165

Ser Ser Ala Asp Ser Cys Asn Met Ser Gly Leu Ile Thr Ile Val
             170              175              180

Val Leu Leu Gly Ile Ala Phe Val Val Tyr Lys Leu Phe Leu Ser
             185              190              195

Asp Gly Gln Tyr Ser Pro Pro Pro Tyr Ser Glu Tyr Pro Pro Phe
             200              205              210

Ser His Arg Tyr Gln Arg Phe Thr Asn Ser Ala Gly Pro Pro Pro
             215              220              225

Pro Gly Phe Lys Ser Glu Phe Thr Gly Pro Gln Asn Thr Gly His
             230              235              240

Gly Ala Thr Ser Gly Phe Gly Ser Ala Phe Thr Gly Gln Gln Gly
             245              250              255

Tyr Glu Asn Ser Gly Pro Gly Phe Trp Thr Gly Leu Gly Thr Gly
             260              265              270

Gly Ile Leu Gly Tyr Leu Phe Gly Ser Asn Arg Ala Ala Thr Pro
             275              280              285

Phe Ser Asp Ser Trp Tyr Tyr Pro Ser Tyr Pro Pro Ser Tyr Pro
             290              295              300

Gly Thr Trp Asn Arg Ala Tyr Ser Pro Leu His Gly Gly Ser Gly
             305              310              315

Ser Tyr Ser Val Cys Ser Asn Ser Asp Thr Lys Thr Arg Thr Ala
             320              325              330

Ser Gly Tyr Gly Gly Thr Arg Arg Arg
             335
```